8-543   198333   ME

From:	Jiang, Dong
Sent:	Thursday, August 10, 2006 8:01 PM
To:	STIC-Biotech/ChemLib
Subject:	10/735,149

Please search SEQ ID NO:28, and 27.

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang
AU1646
REM - 4D70
571-272-0872
Mail stop REM - 4C70

****

Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****

Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:_____
Inventor:_____ Litigation:___

****

Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

THIS PAGE LEFT BLANK

```
Db   382  AAAAAAACCACCCAAAGAAATTCCTAGAAGAAGATTCAAAATCACTTCTCCAAAAAGATGATTCAT 441
          ||||||||  ||  ||  |||||||||||| ||  ||||| || ||| |||||||
Qy   364  CAGCACCTGTCCTCTCGTACCCACCGGTTCCGGAAGAGTTCCGA 405
Db   442  CAGCAATCTGTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA 483
```

RESULT 4
US-09-949-016-4436.
Sequence 4436, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4436
;   LENGTH: 623
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-4436

Query Match   74.0%; Score 299.6; DB 3; Length 623;
Best Local Similarity   84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```
Qy     4  CAAGGTCAAGAATCGCCACACGATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          |||||||||||||||| ||| || ||||| ||  ||||  ||| | ||||||||||||||||
Db   134  CAAGGTCAAGAATCGCCACATGATTAGAATGGGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy    64  AAAAAATTAATGTGAATGAACCTGGTTCCGGGAAATTCCTGCCAGCTCCCGGAAGAGTTGGAGACC 123
          ||||||||| |||| |||| ||||||| | |||||||||||||||||  ||| ||||| |||||
Db   194  AAAAAATTAGTGAATGACCTGGTTCCGGGAAATTCCTGCCAGCTCCCGGAAGAGTTGAGACA 253

Qy   124  AACTGTGAGTGGTCCGCCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
          ||||||||||||||  || ||| ||||||||  ||| |||||  ||  | |||| ||| ||
Db   254  AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTCAGGAAGCCCAACTAAAGTCAGCAAATACA 313

Qy   184  GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAAACGTAAACCGCGTCC 243
          || ||ACAA GAA  ||| |||||| ||||| |||||||| ||||| | |||||||| ||
Db   314  GGAAAACAAATGAAAAGGATTAATCAATGTATCAATTAAAAAGCTGAAGAGAAACCACCTTCC 373

Qy   244  ACCAACGCAGGTCGTCGTCAGAAACACCGTCGACCTGTTGATTCTTATGAG 303
          || || GCAGG  |   | ||| |||||  ||  | |||| ||||||||||
Db   374  ACAAATGCAGGGAGAAGACAGAGAAACACAGACTAACATGCCCTTCAATGTGAATTCTTATGAG 433

Qy   304  AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAAATCCCGCTGCAGAAAATGATTCAC 363
          |||||||| || |||||||||| |||  |||||||||| ||  ||||||||| |||||
Db   434  AAAAAACCACCCAAAGAATTCCTAGAAGAAGATTCAAAATCACTTCTCCAAAAAGATGATTCAT 493

Qy   364  CAGCACCTGTCCTCTCGTACCCACCGGTTCCGGAAGAGTTCCGA 405
          |||||  |||||||| |  || |||||  | ||||  |||| |
Db   494  CAGCAATCTGTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA 535
```

; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 642
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (47)...(532)
US-09-522-217-1

Query Match   74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity   84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```
Qy     4  CAAGGTCAAGAATCGCCACACGATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          |||||||||||||||| ||| || ||||| ||  ||||  ||| | ||||||||||||||||
Db   134  CAAGGTCAAGAATCGCCACATGATTAGAATGGGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy    64  AAAAAATTAATGTGAATGAACCTGGTTCCGGGAAATTCCTGCCAGCTCCCGGAAGAGTTGGAGACC 123
          ||||||||| |||| |||| ||||||| | |||||||||||||||||  ||| ||||| |||||
Db   194  AAAAAATTAATGTGAATGACCTGGTTCCGGGAAATTCCTGCCAGCTCCCGGAAGAGTTGAGACC 253

Qy   124  AACTGTGAGTGGTCCGCCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
          ||||||||||||||  || ||| ||||||||  ||| |||||  ||  | |||| ||| ||
Db   254  AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA 313

Qy   184  GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAAACGTAAACCGCGCGTCC 243
          || ||ACAA GAA  ||| |||||| ||||| |||||||| ||||| | |||||||| ||
Db   314  GGAAACAAATGAAAAGGATTAATCAATGTATCAATTAAAAAGCTGAAGAGAAACCACCTTCC 373

Qy   244  ACCAACGCAGGTCGTCGTCAGAAACACCGTCGTCCTGTTGATTCTTATGAG 303
          || || GCAGG  |   | ||| |||||  ||  | |||| ||||||||||
Db   374  ACAAATGCAGGGAGAAGACAGAGAAACACAGACTAACATGCCCTTCATGTGAATTCTTATGAG 433

Qy   304  AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAAATCCCGTGCAGAAAATGATTCAC 363
          |||||||| || |||||||||| |||  |||||||||| ||  ||||||||| |||||
Db   434  AAAAAACCACCCAAAGAATTCCTAGAAGAAGATTCAAAATCACTTCTCCAAAAAGATGATTCAT 493

Qy   364  CAGCACCTGTCCTCTCGTACCCACCGGTTCCGGAAGAGTTCCGA 405
          |||||  |||||||| |  || |||||  | ||||  |||| |
Db   494  CAGCAATCTGTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA 535
```

RESULT 6
US-09-923-246-1
Sequence 1, Application US/09923246
Patent No. 6605272
GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.

RESULT 5
US-09-522-217-1
Sequence 1, Application US/0952217
Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.

OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: August 7, 2006, 12:10:09 ; Search time 150 Seconds
(without alignments)
5051.994 Million cell updates/sec

Title: US-10-735-149-27
Perfect score: 405
Sequence: 1 atgcaagtcaagatcgcca.........acggttccgaagaattcctga 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues
Database :

Total number of hits satisfying chosen parameters: 2807332

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Database :

Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	299.6	74.0	483	3	US-09-522-217-63	Sequence 63, Appl
2	299.6	74.0	483	3	US-09-923-246-63	Sequence 63, Appl
3	299.6	74.0	483	3	US-10-295-723-63	Sequence 63, Appl
4	299.6	74.0	623	3	US-09-949-016-4436	Sequence 4436, Ap
5	299.6	74.0	642	3	US-09-522-217-1	Sequence 1, Appl
6	299.6	74.0	642	3	US-09-923-246-1	Sequence 1, Appl
7	299.6	74.0	642	3	US-10-295-723-1	Sequence 1, Appl
8	299.6	74.0	486	3	US-10-282-622-1	Sequence 1, Appl
9	299.6	73.2	486	3	US-09-825-561A-9	Sequence 9, Appl
10	294.8	72.8	489	3	US-10-282-622-5	Sequence 5, Appl
11	293.6	72.5	1560	3	US-09-522-217-84	Sequence 84, Appl
12	293.6	72.5	1560	3	US-09-923-246-84	Sequence 84, Appl
13	293.6	72.5	1560	3	US-10-295-723-84	Sequence 84, Appl
14	290.6	71.8	486	3	US-09-522-217-3	Sequence 3, Appli
15	290.6	71.8	486	3	US-09-923-246-3	Sequence 3, Appli
16	290.6	71.8	444	3	US-10-282-622-3	Sequence 3, Appli
17	264.4	65.3	444	3	US-10-295-723-3	Sequence 3, Appli
18	182	44.9	3072	3	US-09-522-217-55	Sequence 55, Appl
19	182	44.9	3072	3	US-09-923-246-55	Sequence 55, Appl
20	182	44.9	3072	3	US-10-295-723-55	Sequence 55, Appl
21	182	44.9	3072	3	US-09-825-561A-46	Sequence 46, Appl
22	175	43.2	1533	3	US-09-522-217-88	Sequence 88, Appl
23	175	43.2	1533	3	US-09-522-246-88	Sequence 88, Appl
24	175	43.2	1533	3	US-10-295-723-88	Sequence 88, Appl
25	105	25.9	12437	3	US-09-949-016-16178	Sequence 16178, A
26	103.4	25.5	1656	3	US-09-522-217-106	Sequence 106, App
27	103.4	25.5	1656	3	US-09-923-246-106	Sequence 106, App
28	103.4	25.5	1656	3	US-10-295-723-106	Sequence 106, App
29	81.4	20.1	1347	3	US-09-522-217-105	Sequence 105, App
30	81.4	20.1	1347	3	US-09-923-246-105	Sequence 105, App
31	81.4	20.1	1347	3	US-10-295-723-105	Sequence 105, App
32	59.6	14.7	535	3	US-09-522-217-4	Sequence 4, Appli
33	59.6	14.7	535	3	US-09-923-246-4	Sequence 4, Appli
34	59.6	14.7	535	3	US-10-295-723-4	Sequence 4, Appli
35	58.8	14.5	645	3	US-09-522-217-108	Sequence 108, App
36	58.8	14.5	645	3	US-09-923-246-108	Sequence 108, App
37	58.8	14.5	645	3	US-10-295-723-108	Sequence 108, App
38	44.4	11.0	601	3	US-09-949-016-158662	Sequence 158662,
39	35.2	8.7	404465	3	US-09-949-016-12561	Sequence 12561, A
40	32	7.9	1600	3	US-09-949-016-4038	Sequence 4038, A
41	32	7.9	12113	3	US-09-949-016-15144	Sequence 15144, A
42	32	7.9	13445	3	US-09-949-016-15780	Sequence 15780, A
43	31.6	7.8	73853	3	US-09-949-016-12029	Sequence 12029, A
44	31.4	7.8	1230230	3	US-09-438-185A-1	Sequence 1, Appli
45	31.2	7.7	6819	3	US-09-949-016-12457	Sequence 12457, A

ALIGNMENTS

RESULT 1
US-09-522-217-63
Sequence 63, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 483
TYPE: DNA
ORGANISM: homo sapiens
US-09-522-217-63

Query Match 74.0%;   Score 299.6;   DB 3;   Length 483;
Best Local Similarity 84.1%;   Pred. No. 2.6e-87;
Matches 338;   Conservative 0;   Mismatches 64;   Indels 0;   Gaps 0;

```
Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGCCGTCAACTTATAGAATATTGTTGATCAGCTG   63
         ||||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Db   82 CAAGGTCAAGATCGCCACACTGATTAGAATGCCGTCAACTTATAGAATATTGTTGATCAGCTG  141

Qy   64 AAAAATTATGTGAATGACCTGTTCCGGAATTCCTGCGGCTTCCGGAAGAGATGTTGAGACC  123
         ||||||||||||||||||   ||| ||  || ||| |||| ||| ||||| |||| ||||
Db  142 AAAAATTATGTGAATGACTTGGTCTCCTGGTCCCGAATTCTCTGCCAGCTCCAGAAGAGTGTTAGAGACA  201

Qy  124 AACTGTGAGTGGTCCGCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAACACC  183
```

Db   202 AACTGTGAGTGGTGCAGCTTTTTCCTGTTTTTCAGAGAGGCCCAACTAAAGTCAGCAAATACA 261
Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTTAAACCCGCGTCC 243
Db   262 GGAAACAATGAAAAGGATAATCAATCTATCAATTAAAAAGCTGAGAGAAAACACACTTCC 321
Qy   244 ACCAACGCAGGTCGTCGTCGAGAAAACACCGGTCTGACCTGCCCGTCTCTGATTCTTATGAG 303
Db   322 ACAAATGCAGGGAGGAAGAGACAGAAAACACACTAACACTGCCCTTCATGTGATTCTTATGAG 381
Qy   304 AAAAAACCCGCGAAAGAATTCCTGCTGCAGAAAATGATTCAC 363
Db   382 AAAAAAACCACCCAAAGAAGAATTCAAATCACTTCTCCAAAAAGATGAATTCAT 441
Qy   364 CACGCACCTGTCCTCCTCGTACCCACAGGGTTCCGGAAGAATTCCTGA 405
Db   442 CAGCAATCTGTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA 483

RESULT 2
US-09-923-246-63
; Sequence 63, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; SEQ ID NO 63
;   LENGTH: 483
;   TYPE: DNA
;   ORGANISM: homo sapiens
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
US-09-923-246-63

Query Match   74.0%; Score 299.6; DB 3; Length 483;
Best Local Similarity   84.1%; Pred. No. 2.6e-87;
Matches 338; Conservative   0; Mismatches 64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCCGCCACATGATTAGAAATGCGGTCAACTTATAGAATATTGTTGATCAGCTG 63
Db   82 CAAGGTCAAGATCCGCCACATGATTAGAAATCGGTCAACTTATAGATATTGTTGATCGCTG 141
Qy   64 AAAAATTATGTGAATGAACCTGGGTTCCGGGAATTCCTGCCGGCCTCCGGAAGAGTTGAGACC 123
Db   142 CAAGGTCAAGATCCCACATGATTAGAATCGGTCAACTTATAGATATTGTTGATCGCTG 201
Qy   124 AAAAATTATGTGAATGAACCTGGGTTCCGGGAATTCCTGCCGGCCTCCGGAAGAGTTGAGACC 183
Db   202 AACTGTGAGTGGTGCAGCTTTTTCCTGTTTTCCTGTTTTCAGAGAGGCCCAACTAAAGTCAGCAAATACA 261
Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTTAAACCCGCGTCC 243
Db   262 GGAAACAATGAAAAGGATAATCAATCTATCAATTAAAAAGCTGAGAGAAAACACACTTCC 321
Qy   244 ACCAACGCAGGTCGTCGTCGAGAAAACACCGGTCTGACCTGCCCGTCTCTGATTCTTATGAG 303
Db   322 ACAAATGCAGGGAGGAAGAGACAGAAAACACACTAACACTGCCCTTCATGTGATTCTTATGAG 381
Qy   304 AAAAAACCCGCGAAAGAATTCCTGCTGCAGAAAATGATTCAC 363
Db   382 AAAAAAACCACCCAAAGAAGAATTCAAATCACTTCTCCAAAAAGATGAATTCAT 441
Qy   364 CACGCACCTGTCCTCCTCGTACCCACAGGGTTCCGGAAGAATTCCTGA 405
Db   442 CAGCAATCTGTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA 483

Qy   244 ACCAACGCAGGTCGTCGTCGAGAAAACACCGGTCTGACCTGCCCGTCTCTGATTCTTATGAG 303
Db   322 ACAAATGCAGGGAGGAAGAGACAGAAAACACACTAACACTGCCCTTCATGTGATTCTTATGAG 381
Qy   304 AAAAAACCCGCGAAAGAATTCCTGCTGCAGAAAATGATTCAC 363
Db   382 AAAAAAACCACCCAAAGAAGAATTCAAATCACTTCTCCAAAAAGATGAATTCAT 441
Qy   364 CACGCACCTGTCCTCCTCGTACCCACAGGGTTCCGGAAGAATTCCTGA 405
Db   442 CAGCAATCTGTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA 483

RESULT 3
US-10-295-723-63
; Sequence 63, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; SEQ ID NO 63
;   LENGTH: 483
;   TYPE: DNA
;   ORGANISM: homo sapiens
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
US-10-295-723-63

Query Match   74.0%; Score 299.6; DB 3; Length 483;
Best Local Similarity   84.1%; Pred. No. 2.6e-87;
Matches 338; Conservative   0; Mismatches 64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCCGCCACATGATTAGAAATGCGGTCAACTTATAGAATATTGTTGATCAGCTG 63
Db   82 CAAGGTCAAGATCCGCCACATGATTAGAAATCGGTCAACTTATAGATATTGTTGATCGCTG 141
Qy   64 AAAAATTATGTGAATGAACCTGGGTTCCGGGAATTCCTGCCGGCCTCCGGAAGAGTTGAGACC 123
Db   142 AAAAATTATGTGAATGACCTGGTTCCGGGAATTCCTGCCCAGCTCCAGAAGAGTTAGAGACA 201
Qy   124 AACTGTGAGTGGTGCAGCTTTTTCCTGTTTTCCTGTTTTCAGAGAGGCCCAACTAAAGTCAGCAAATACA 183
Db   202 AACTGTGAGTGGTGCAGCTTTTTCCTGTTTTCAGAGAGGCCCAACTAAAGTCAGCAAATACA 261
Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTTAAACCCGCGTCC 243
Db   262 GGAAACAATGAAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGAAAACACACTTCC 321
Qy   244 ACCAACGCAGGTCGTCGTCGAGAAAACACCGGTCTGACCTGCCCGTCTCTGATTCTTATGAG 303
Db   322 ACAAATGCAGGGAGGAAGAGACAGAAAACACACTAACACTGCCCTTCATGTGATTCTTATGAG 381
Qy   304 AAAAAACCCGCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363

RESULT 4
US-09-949-016-4436
; Sequence 4436, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4436
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4436

Query Match   74.0%; Score 299.6; DB 3; Length 623;
Best Local Similarity   84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative   0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGAATCGCCACATGATTAGAATGAGATGGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAAATTATGTGAATGACCTGGTTCCCGGAATTCCTGCCGGTCCGGAAGAGATGTTGAGACC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCGAAAAGCCCAGCTGAAATCCCAAACACC 253

Qy   124 AACTGTGAGTGGTCCGGCTTTCTCCTGTTTCCAGAAAAAGCCCAGCTGAAATCCGCAAACACC 183
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTCAGAAGGCCCCAACTAAAGTCACGCAAAATACA 313

Qy   184 GGTAACAACGAAACGTATCATCAACGTTTCCATTAAAAAACTGAAAAGTAAACCGCGCGTCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAAACAATGAAAGGATAAATCAAATGTATCAAATTAAAAAAGCTGAAGAGAGGAAACCACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCTCCGTCCTGTGATTCTTTATGAG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ACAAATGCAGGGAGAGACAGAAACAGACTAACAGCGCCTTCACTTCTCCAAAAGATGATTCAC 433

Qy   304 AAAAAAACCGCCGAAAAGAATTCCTGGAAGCGGTTTCAAATCCCTGCTGCGAGAAAAATGATTCAC 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAAACCACCCAAAGAATTCCTAGAAACAACACGGAAGTGAAGAATTCCTGA 493

Qy   364 CAGCACCTGTCCTCTGTTCCGAAGATTCCTGA 405
          |||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAATTCCTGA 535

RESULT 5
US-09-522-217-1
; Sequence 1, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.

Qy   382 AAAAAACCACCCAAAGAATTCCTAGAAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT 441
          || || |||||||||| ||| | || |||||| ||| || ||| || ||||||||||||
Qy   364 CAGCACCTGTCCTCTCGTTCCACGGTTCCGAAGATTCCTGA 405
          ||||| ||||||||||||| ||||||||||||||||||
Db   442 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAATTCCTGA 483

RESULT 6
US-09-923-246-1
; Sequence 1, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.

; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-09-522-217-1

Query Match   74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity   84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative   0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGAATCGCCACATGATTAGAATGAGATGGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGCCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAAATTATGTGAATGACCTGGTTCCCGGAATTCCTGCCGGTCCGGAAGAGATGTTGAGACC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCGAAAAGCCCAGCTGAAATCCCAAACACC 253

Qy   124 AACTGTGAGTGGTCCGGCTTTCTCCTGTTTCCAGAAAAAGCCCAGCTGAAATCCGCAAACACC 183
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTCAGAAGGCCCCAACTAAAGTCACGCAAAATACA 313

Qy   184 GGTAACAACGAAACGTATCATCAACGTTTCCATTAAAAAACTGAAAAGTAAACCGCGCGTCC 243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAAACAATGAAAGGATAAATCAAATGTATCAAATTAAAAAAGCTGAAGAGAGGAAACCACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCTCCGTCCTGTGATTCTTTATGAG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ACAAATGCAGGGAGAGACAGAAACAGACTAACAGCGCCTTCACTTCTCCAAAAGATGATTCAC 433

Qy   304 AAAAAAACCGCCGAAAAGAATTCCTGGAAGCGGTTTCAAATCCCTGCTGCGAGAAAAATGATTCAC 363
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAAACCACCCAAAGAATTCCTAGAAACAACACGGAAGTGAAGAATTCCTGA 493

Qy   364 CAGCACCTGTCCTCTCGTTCCGTACCCACGGTTCCGAAGATTCCTGA 405
          ||||| ||||||||||||| ||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAATTCCTGA 535

; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-09-923-246-1

Query Match   74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity   84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative   0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAATTATGTGAATGAATCCGTCCCGGAATTCCTGCCGCGGAAGATGTTGAGACC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAATTATGTGAATGAATCCGTCCCGGAATTCCTGCCGCGGAAGATGTTGAGACC 253

Qy   124 AACTGTGAGTGGTCCGGCTTTCTCCCGTGTTTTCCAGAAAAGCCCAGCTGAAATCCGCAAACACC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTTCCGTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA 313

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAACAACATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAAGAGGAAACCACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTCTGACCTGCGAAAACACCGTCTGACCTGCCCTGTGATTCTTATGAG 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ACAAATGCAGGGAGGAGGAAGACAGAAAACACAGACTAACATGCCCTTCATCGTGATTCTTATGAG 433

Qy   304 AAAAAAACCGCGGAAAAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAAACCACCCAAAGAATTCCTAGAAAAGAATTCAAATCACTTCTCCAAAAAGATGATTCAT 493

Qy   364 CAGCACCTGTCCTCCTCGTTACCCACGGTTCCGAAGATTCCTGA 405
          ||||||||||||||||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 535

RESULT 7
US-10-295-723-1
; Sequence 1, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-295-723-1

Query Match   74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity   84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative   0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAATTATGTGAATGAATCCGTCCCGGAATTCCTGCCGCGGAAGATGTTGAGACC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAATTATGTGAATGAATCCGTCCCGGAATTCCTGCCGCGGAAGATGTTGAGACA 253

Qy   124 AACTGTGAGTGGTCCGGCTTTCTCCCGTGTTTTCCAGAAAAGCCCAGCTGAAATCCGCAAACACC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTTCCGTGTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA 313

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAAGAGGAAACCACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTCTGACCTGCGAAAACACCGTCTGACCTGCCCTTCATCGTGATTCTTATGAG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ACAAATGCAGGGAGGAGGAAGACAGAAAACACAGACTAACATGCCCTTCATCGTGATTCTTATGAG 433

Qy   304 AAAAAAACCGCGGAAAAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAAACCACCCAAAGAATTCCTAGAAAAGAATTCAAATCACTTCTCCAAAAAGATGATTCAT 493

Qy   364 CAGCACCTGTCCTCCTCGTTACCCACGGTTCCGAAGATTCCTGA 405
          ||||||||||||||||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 535

RESULT 8
US-10-282-622-1
; Sequence 1, Application US/10282622
; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. 6929932ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1

```
;  LENGTH: 642
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (47)...(532)
US-10-282-622-1

Query Match          74.0%;  Score 299.6;  DB 3;  Length 642;
Best Local Similarity  84.1%;  Pred. No. 2.9e-87;
Matches 338;  Conservative   0;  Mismatches  64;  Indels  0;  Gaps  0;

Qy    4 CAAGGTCAAGATCGCCACATGAATGCGTCAACTTATAGAATATTGTTGATCAGCTG 63
          |||||||||||||||||||||   ||||||||||||||| ||||||||||||||||
Db  134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAAATTATGTGAATGAATGACCTGGTTCCGGAAATTCCTGCGCGGGAAGATGTTGAGACC 123
          ||||||||||||||||||||||| ||||||   |||||| || |  |||   |||||| |||||
Db  194 AAAAAATTATGTGAATGAATGACTTGGTTCCCTGAAATTCTGCCCAGCTCCAGAAGATGTTAGAGACA 253

Qy  124 AACTGTGAGTGGTGTCCCGCTTTCTCCCGTTTCCAGAAAGCCCACTGAAATCCCAAACACC 183
          ||||||||||||||||   |||||  || ||||| |||| |||| || |||| |||| ||| 
Db  254 AACTGTGAGTGGTGTCAGCTTTTTCCTGTTTTTCAGAAGCCCCAACTAAAGTCAGCAAATACA 313

Qy  184 GGTAACAACGAACGTATCATCAAACGTTTCCATTAAAAAAACTGAAACGTAAACCGCGTCC 243
          || ||||| | ||   ||||| |||| | |  ||||||| ||||||  | |||| | ||| ||
Db  314 GGAAACAAATGAAAAGGATTAATCAATTGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC 373

Qy  244 ACCAACGCAGGTCGTCGTCAGAAAACACGACTAACATGCCCTTCATGTGATTCTTATGAG 303
          ||  | |||||  | |  |||||||||| |||||||| ||  || ||   ||| |||
Db  374 ACAAATGCAGGGAGAAGACAGAAAAACAAGACTAACATCAATTAAAAAGATGAAATGATTCAC 433

Qy  304 AAAAAACCGCGAAAGAATTCCTGGAAGCGTTTCAAAATCCCTGCTGCCAGCAGAAAATGATTCAC 363
          |||||||| | |||||||||||  |||  |||||||||| ||   |    ||| |||| ||||| 
Db  434 AAAAAACCACCCAAAGAATTCCTAGAAAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT 493

Qy  364 CAGCACCTGTCCTCTCGTACCCACACGGTTCCGAAGATTCCTGA 405
          ||||| |||||||||  | ||||||||  | |||||||||||||
Db  494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAATTCCTGA 535
```

```
RESULT 9
US-09-825-561A-9
;  Sequence 9, Application US/0982556IA
;  Patent No. 6777539
;  GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT: No. 6777539ak, Julia E.
;  APPLICANT: West, James W.
;  APPLICANT: Presnell, Scott R.
;  APPLICANT: Holly, Richard D.
;  APPLICANT: Nelson, Andrew J.
;  TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
;  FILE REFERENCE: 00-22
;  CURRENT APPLICATION NUMBER: US/09/825,561A
;  CURRENT FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/194,731
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/222,121
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
;  LENGTH: 486
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(486)
US-09-825-561A-9

Query Match          73.2%;  Score 296.6;  DB 3;  Length 486;
Best Local Similarity  84.0%;  Pred. No. 2.4e-86;
```

```
Matches 335;  Conservative   0;  Mismatches  64;  Indels  0;  Gaps  0;

Qy    4 CAAGGTCAAGATCGCCACATGAATGCGTCAACTTATAGAATATTGTTGATCAGCTG 63
          |||||||||||||||||||||   ||||||||||||||| ||||||||||||||||
Db   88 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 147

Qy   64 AAAAAATTATGTGAATGAATGACCTGGTTCCGGAAATTCCTGCGCGGGAAGATGTTGAGACC 123
          ||||||||||||||||||||||| ||||||   |||||| || |  |||   |||||| |||||
Db  148 AAAAAATTATGTGAATGAATGACTTGGTTCCCTGAAATTCTGCCCAGCTCCAGAAGATGTTAGAGACA 207

Qy  124 AACTGTGAGTGGTGTCCCGCTTTCTCCCGTTTCCAGAAAGCCCACTGAAATCCCAAACACC 183
          ||||||||||||||||   |||||  || ||||| |||| |||| || |||| |||| ||| 
Db  208 AACTGTGAGTGGTGTCAGCTTTTTCCTGTTTTTCAGAAGCCCCAACTAAAGTCAGCAAATACA 267

Qy  184 GGTAACAACGAACGTATCATCAAACGTTTCCATTAAAAAAACTGAAACGTAAACCGCGTCC 243
          || ||||| | ||   ||||| |||| | |  ||||||| ||||||  | |||| | ||| ||
Db  268 GGAAACAAATGAAAGGATTAATCAATTGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC 327

Qy  244 ACCAACGCAGGTCGTCGTCAGAAAACACGACTAACATGCCCTTCATGTGATTCTTATGAG 303
          ||  | |||||  | |  |||||||||| |||||||| ||  || ||   ||| |||
Db  328 ACAAATGCAGGGAGAAGACAGAAAAACAAGACTAACATCAATTAAAAAGATGAAATGATTCAC 387

Qy  304 AAAAAACCGCGAAAGAATTCCTGGAAGCGTTTCAAAATCCCTGCTGCAGCAGAAAATGATTCAC 363
          |||||||| | |||||||||||  |||  |||||||||| ||   |    ||| |||| ||||| 
Db  388 AAAAAACCACCCAAAGAATTCCTAGAAAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT 447

Qy  364 CAGCACCTGTCCTCTCGTACCCACACGGTTCCGAAGATTCC 402
          ||||| |||||||||  | ||||||||  | |||||||||
Db  448 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAATTCC 486
```

```
RESULT 10
US-10-282-622-5
;  Sequence 5, Application US/10282622
;  Patent No. 6929932
;  GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT: West, James W.
;  APPLICANT: No. 6929932ak, Julia E.
;  TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
;  FILE REFERENCE: 01-37
;  CURRENT APPLICATION NUMBER: US/10/282,622
;  CURRENT FILING DATE: 2002-10-28
;  PRIOR APPLICATION NUMBER: 60/337,586
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
;  LENGTH: 489
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: zalpha11 ligand Q153D/I156D
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(489)
US-10-282-622-5

Query Match          72.8%;  Score 294.8;  DB 3;  Length 489;
Best Local Similarity  83.3%;  Pred. No. 9.4e-86;
Matches 335;  Conservative   0;  Mismatches  67;  Indels  0;  Gaps  0;

Qy    4 CAAGGTCAAGATCGCCACATGAATGCGTCAACTTATAGAATATTGTTGATCAGCTG 63
          |||||||||||||||||||||   ||||||||||||||| ||||||||||||||||
Db    4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63

Qy   64 AAAAAATTATGTGAATGAATGACCTGGTTCCGGAAATTCCTGCGCGGGAAGATGTTGAGACC 123
          ||||||||||||||||||||||| ||||||   |||||| || |  |||   |||||| |||||
Db   64 AAAAAATTATGTGAATGAATGACTTGGTTCCCTGAAATTCTGCCCAGCTCCAGAAGATGTTAGAGACA 123

Qy  124 AACTGTGAGTGGTGTCCCGCTTTCTCCCGTTTCCAGAAAGCCCAGTTGAAATCCGCAAAACACC 183
          |||||||||||||||   |||||  || ||||| |||| |||| || |||| |||| ||| 
Db  148 AACTGTGAGTGGTGTCAGCTTTTTCCTGTTTTTCAGAAGCCCCAACTAAAGTCAGCAAATACA 267
```

RESULT 11
US-09-522-217-84
; Sequence 84, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1560)
; OTHER INFORMATION: MBP-human zalpha11 Ligand fusion polynucleotide
US-09-522-217-84

  Query Match   72.5%; Score 293.6; DB 3; Length 1560;
  Best Local Similarity   83.8%; Pred. No. 4.1e-85;
  Matches 332; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   10 CAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTGAAAAAT 69
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 CAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTGAAAAAT 1224

Qy   70 TATGTGAATGAACCTGGCTTCCGGCTTATGATATTCTGCCAGCTCCAGAAGAGATGTTGT 129
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 TATGTGAATGAACTTGGTCCCTGAAATTTCTGCCAGCGTAGAGACCAAACTGT 1284

Qy   130 GAGTGGTCCGCCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGGAAACACCGGTAAC 189
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 GAGTGGTCAGCTTTTTCCTGTTTCCAGAAGGCCCAACTCAGCAAATACACAGGAAAC 1344

Qy   190 AACGAAACGTATCATCAACGTTTCATTAAAAAACTGAAAACGCCGTCCACCAAC 249
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 GAGTGGTCAGCTTTTTCCTGTTTCCAGAAGGCCCAACTCAGCAAATACACAGGAAAC 1344

RESULT 12
US-09-923-246-84
; Sequence 84, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1560)
; OTHER INFORMATION: MBP-human zalpha11 Ligand fusion polynucleotide
US-09-923-246-84

  Query Match   72.5%; Score 293.6; DB 3; Length 1560;
  Best Local Similarity   83.8%; Pred. No. 4.1e-85;
  Matches 332; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   10 CAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTGAAAAAT 69
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 CAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTGAAAAAT 1224

Qy   70 TATGTGAATGAACCTGGCTTCCGGCTTATGATATTCTGCCAGCTCCAGAAGAGATGTTGT 129
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 TATGTGAATGACTTGGTCCCTGAAATTTCTGCCAGCGTAGAGACCAAACTGT 1284

Qy   130 GAGTGGTCCGCCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGGAAACACCGGTAAC 189
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 GAGTGGTCAGCTTTTTCCTGTTTCCAGAAGGCCCAACTCAGCAAATACACAGGAAAC 1344

Qy   190 AACGAAACGTATCATCAACGTTTCATTAAAAAACTGAAAACGCCGTCCACCAAC 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345 AATGAAAGGATAATTCAATGTATCAATTAAAAAAGCTGAAGAGAGGAAAACCAACTT 1404

Qy   250 GCAGGTCGTCGTCAGAAAACACCGTCTGACCTGCCGTCCCTGTCTGATTCTTATGAGAAAA 309
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345 AATGAAAGGATAATTCAATGTATCAATTAAAAAAGCTGAAGAGAGGAAAACCAACTT 1404

```
Db   1405  GCAGGGAGGAAGACAGAGAAACACAGACTAACACATGCCCTTCAATGTGATTCTTTATGAGAAAAA 1464
                |||||  | |||||||  ||||||||| ||||||| |||||||  || ||||||||||||||||||
Qy    310  CCGCCGAAAGAGAATTCCTTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCACCAGCAC 369
Db   1465  CCACCCAAAAGAATTCCTTAGAAAGATTCAAATCACTTCTTCCAAAAAGATGATTCATCAGCAT 1524
                ||||||||||  ||||||| ||||||| ||||||  ||  ||||||||||||  ||| ||||
Qy    370  CTGTCCTTCTCGTTACCCACGGGTTCCGGAAGATTCCTGA 405
Db   1525  CTGTCCTTCTTAGAACACACACGGGAGTGAAGAATTCCTGA 1560
```

```
RESULT 13
US-10-295-723-84
; Sequence 84, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
;   APPLICANT: No. 6686178ak, Julia E.
;   APPLICANT: Presnell, Scott R.
;   APPLICANT: Sprecher, Cindy A.
;   APPLICANT: Foster, Donald C.
;   APPLICANT: Holly, Richard D.
;   APPLICANT: Gross, Jane A.
;   APPLICANT: Johnston, Janet V.
;   APPLICANT: Nelson, Andrew J.
;   APPLICANT: Dillon, Stacey R.
;   APPLICANT: Hammond, Angela K.
;   TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;   FILE REFERENCE: 99-16
;   CURRENT APPLICATION NUMBER: US/10/295,723
;   CURRENT FILING DATE: 2002-11-15
;   PRIOR APPLICATION NUMBER: 09/522,217
;   PRIOR FILING DATE: 2000-03-09
;   PRIOR APPLICATION NUMBER: US 60/123,547
;   PRIOR FILING DATE: 1999-03-09
;   PRIOR APPLICATION NUMBER: US 60/123,904
;   PRIOR FILING DATE: 1999-03-11
;   PRIOR APPLICATION NUMBER: US 60/142,013
;   PRIOR FILING DATE: 1999-07-01
;   NUMBER OF SEQ ID NOS: 115
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 84
;   LENGTH: 1560
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1560)
;   OTHER INFORMATION: MBP-human zalpha11 ligand fusion polynucleotide

  Query Match             72.5%;  Score 293.6;  DB 3;  Length 1560;
  Best Local Similarity   83.8%;
  Matches  332;  Conservative   0;  Mismatches  64;  Indels   0;  Gaps   0;

Qy     10  CAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTGAAAAAT 69
               ||||| |||||||||||||||||||| ||||||||||||||||||||||| |||||||
Db   1165  CAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTGAAAAAT 1224
Qy     70  TATGTGAATGACCTGGTTCCGGAATTCCTGCCGCGGCTCCGGAAGATGTTGAGACCAACTGT 129
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225  TATGTGAATGACCTGGTTCCGGAATTCTCTGCCGAGCTCCCAGAAGAGTAGAGACAAAACTGT 1284
Qy    130  GAGTGGTCCGGCTTTCTCCGTGTTTCCAGAAGCCCAGCTGAAATCCGCAAACACCGGTAAC 189
               |||||||||| ||||||||||||||||||| ||||||||| |||||||||||||| ||
Db   1285  GAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAGAAATACAGGAAAC 1344
Qy    190  AACGAACGTATCATCAACGTTTCCATTAAAAAAACGTAAACACACCGGTCCCGTCCCACAAC 249
               ||||||| |||| ||||  ||||||| ||||  |||||| || ||||||  ||||  ||
Db   1345  AATGAAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCCACAAAT 1404
Qy    250  GCAGGTCGTCGTCAGAAACACCGTCTCGACCTGCCCGTCCTGTGAATTCTTATGAGAAAAA 309
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1405  GCAGGGAGGAAGACAGAGAAACACAGACTAACACATGCCCTTCAATGTGATTCTTTATGAGAAAAA 1464
```

```
Db   1405  GCAGGGAGGAAGACAGAGAAACACAGACTAACACATGCCCTTCAATGTGATTCTTTATGAGAAAAA 1464
                |||||  | |||||||  ||||||||| ||||||| |||||||  || ||||||||||||||||||
Qy    310  CCGCCGAAAGAGAATTCCTTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCACCAGCAC 369
Db   1465  CCACCCAAAAGAATTCCTTAGAAAGATTCAAATCACTTCTTCCAAAAAGATGATTCATCAGCAT 1524
                ||||||||||  ||||||| ||||||| ||||||  ||  ||||||||||||  ||| ||||
Qy    370  CTGTCCTTCTCGTTACCCACGGGTTCCGGAAGATTCCTGA 405
Db   1525  CTGTCCTTCTTAGAACACACACGGGAGTGAAGAATTCCTGA 1560
```

```
RESULT 14
US-09-522-217-3
; Sequence 3, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
;   APPLICANT: No. 6307024ak, Julia E.
;   APPLICANT: Presnell, Scott R.
;   APPLICANT: Sprecher, Cindy A.
;   APPLICANT: Foster, Donald C.
;   APPLICANT: Holly, Richard D.
;   APPLICANT: Gross, Jane A.
;   APPLICANT: Johnston, Janet V.
;   APPLICANT: Nelson, Andrew J.
;   APPLICANT: Dillon, Stacey R.
;   APPLICANT: Hammond, Angela K.
;   TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
;   FILE REFERENCE: 99-16
;   CURRENT APPLICATION NUMBER: US/09/522,217
;   CURRENT FILING DATE: 2000-03-09
;   EARLIER APPLICATION NUMBER: US 60/123,547
;   EARLIER FILING DATE: 1999-03-09
;   EARLIER APPLICATION NUMBER: US 60/123,904
;   EARLIER FILING DATE: 1999-03-11
;   EARLIER APPLICATION NUMBER: US 60/142,013
;   EARLIER FILING DATE: 1999-07-01
;   NUMBER OF SEQ ID NOS: 115
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 486
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Degenerate polynucleotide sequence for human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(486)
;   OTHER INFORMATION: n = A,T,C or G
US-09-522-217-3

  Query Match             71.8%;  Score 290.6;  DB 3;  Length 486;
  Best Local Similarity   56.5%;
  Matches  225;  Conservative  114;  Mismatches  59;  Indels   0;  Gaps   0;

Qy      4  CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
               ||||| : |||||||||||||||||:||| |::||||||:|||||:|||||:||||||:
Db     88  CARGGNCARGAYMCNCAVATGAYMGNATGMGNCARYTNATHGAYATHGTNGAYCARYTN 147
Qy     64  AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGCGGCTCCGGAAGATGTTGAGACC 123
               ||| |:: ||:::||::||:::||||:::|||::|:||:|:|::::||:||:||::||||
Db    148  AARAAYTAYGTNAAYGAYYTNGTNCCNGARTYYYTNCCNGCNCGNGARGAYGTNGARACN 207
Qy    124  AACTGTGAGTGGTCCGGCTTTCTCCGTGTTTCCAGAAGCCCAGCTGAAATCCGCAAACACC 183
               |||:||:||:||:||::|||:||:||:||::||||||:|||:|||:|||:|:||:|||||:
Db    208  AAYTGYGARTGGWSNGGNCNTTYWSNTGYYTNYCARAARGGNCARYTNAARWSNGCNAAYACN 267
Qy    184  GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAGCGTAAACACCGGTCC 243
               ||:||:||:||::|:|:|:|:||:||:::||||||||||||:||||:::|||||:|||:||
Db    268  GGNAAYAAYGARMGNATHATHAAYGTNWSNATHAARAARAYTNAARMGNAARCNCNCNWSN 327
Qy    244  ACCAACGCAGGTCGTCGTCAGAAACACCGTCTCGACCTGCCCGTCCTGTGAATTCTTATGAG 303
               |||:|| ||||:||:||:|||||||||||:||:||:||:||:||:||:||:||||||||||
```

```
Db   328  ACNAAYGCNGNGMGNMGNCARARAARCAYMGNYTNACNTGYCNWSNTGYGAYWSNTAYGAR  387

Qy   304  AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC  363
          |||:||:|||:::|||||||||||:||||||:|||||:|:||||||:||||||||||||||
Db   388  AARAAARCCNCCNAARGARTTYYTNGARMGNTTYAARWSNYTNYTNCARARARATGATHCAY  447

Qy   364  CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTC  401
          |||:|||||:||:|||:||:||:||||:||||||:|||
Db   448  CARCAYYTNWSNWSNMGNACNCAYGGNWSNGARGAYWS  485
```

RESULT 15

US-09-923-246-3

; Sequence 3, Application US/09923246

; Patent No. 6605272

; GENERAL INFORMATION:

;   APPLICANT: No. 6605272ak, Julia E.

;   APPLICANT: Presnell, Scott R.

;   APPLICANT: Sprecher, Cindy A.

;   APPLICANT: Foster, Donald C.

;   APPLICANT: Holly, Richard D.

;   APPLICANT: Gross, Jane A.

;   APPLICANT: Johnston, Janet V.

;   APPLICANT: Nelson, Andrew J.

;   APPLICANT: Dillon, Stacey R.

;   APPLICANT: Hammond, Angela K.

;   TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

;   FILE REFERENCE: 99-16

;   CURRENT APPLICATION NUMBER: US/09/923,246

;   CURRENT FILING DATE: 2001-08-03

;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

;   PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

;   NUMBER OF SEQ ID NOS: 115

;   SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 3

;   LENGTH: 486

;   TYPE: DNA

;   ORGANISM: Artificial Sequence

;   FEATURE:

;   OTHER INFORMATION: Degenerate polynucleotide sequence for human

;   OTHER INFORMATION: zalpha11 ligand

;   NAME/KEY: misc_feature

;   LOCATION: (1)..(486)

;   OTHER INFORMATION: n = A,T,C or G

US-09-923-246-3

Query Match   71.8%; Score 290.6; DB 3; Length 486;
Best Local Similarity   56.5%; Pred. No. 2.2e-84;
Matches 225; Conservative 114; Mismatches 59; Indels 0; Gaps 0;

```
Qy     4  CAAGGTCAAGATCGCCACAATGATTAGAATCGTCAACTTATAGATATTGTTGATCAGCTG  63
          ||||||:||||:||:|||||:|||||||:||:|||||||:||:|||||:||||||||||:
Db    88  CARGGNCARGAYMGNCAYATGATHMGNATCGNCARYTNATHGAVATHGTNGAYCARYTN  147

Qy    64  AAAAAATTATGTGAATGACCTGGGTTCCGGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC  123
          ||:||||||||:|||:||||:||||:||:|||||||||||:||||||:||||||:||||||||
Db   148  AARAAAYTAYGTNAAYGAYYTNGTNCNGARYTYYTNCNGARGAYGTNGARACN  207

Qy   124  AACTGTGAGTGGTCCGCCTTTCTCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC  183
          |||||||||:||:||:||||:||:|||||||||||:|||||||:||||||:|||||:|||
Db   208  AAYTGYGARYGGWSNGCNTTYWSNTGYTTYCARAARGCNCARYTNAARWSNGCNAAYACN  267

Qy   184  GGTAACAACAACGTATCATCAACGTTTCATTAAAAAAACTGAAACGTAAACGCGCGTCC  243
          ||:||:||:||:||:||:||||||||:|||||:|||||||:|||||:|||||:|||:||
Db   268  GGNAAYAAYGARMGNATHATHAAYGTNWSNATHARAARYTNAARMGNAARCCNCNCNWSN  327

Qy   244  ACCAACGCACAGGTCGTCGTCAGAAAAACACCGTCTGACCTGCCCGTCCTGTGAATTCTTATGAG  303
          |||:||:|||||:||:|||:|||||||||||:||:|:||:||||||:||||:||:||:||||:||
Db   328  ACNAAYGCNGNGMGNMGNCARARAARCAYMGNYTNACNTGYCNWSNTGYGAYWSNTAYGAR  387
```

```
Qy   304  AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC  363
          |||:||:|||:::|||||||||||:||||||:|||||:|:||||||:||||||||||||||
Db   388  AARAAARCCNCCNAARGARTTYYTNGARMGNTTYAARWSNYTNYTNCARARARATGATHCAY  447

Qy   364  CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTC  401
          |||:|||||:||:|||:||:||:||||:||||||:|||
Db   448  CARCAYYTNWSNWSNMGNACNCAYGGNWSNGARGAYWS  485
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration ltd.

Run on: August 7, 2006, 12:13:07 ; Search time 1011 Seconds
                 (without alignments)
                 4922.346 Million cell updates/sec

Title: US-10-735-149-27
Perfect score: 405
Sequence: 1 atgcaaggtcaagatccgcca.........acggttccgaagattcctga 405

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA_Main:*
           1:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
           2:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
           3:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
           4:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
           5:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
           6:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
           7:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
           8:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
           9:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
          10:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
          11:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
          12:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
          13:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
          14:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
          15:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
          16:    /EMC_Celera_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	299.6	74.0	483	3	US-09-923-246-63	Sequence 63, Appl
2	299.6	74.0	483	7	US-10-295-723-63	Sequence 63, Appl
3	299.6	74.0	483	8	US-10-659-684-63	Sequence 63, Appl
4	299.6	74.0	483	9	US-10-787-442-63	Sequence 63, Appl
5	299.6	74.0	489	10	US-10-775-204-2157	Sequence 2157, Ap
6	299.6	74.0	642	3	US-09-923-246-1	Sequence 1, Appli
7	299.6	74.0	642	7	US-10-295-723-1	Sequence 1, Appli
8	299.6	74.0	642	8	US-10-282-622-1	Sequence 1, Appli
9	299.6	74.0	642	9	US-10-456-780-1	Sequence 1, Appli
10	299.6	74.0	642	10	US-10-659-684-1	Sequence 1, Appli
11	299.6	74.0	642	9	US-10-787-442-1	Sequence 1, Appli
12	299.6	74.0	642	10	US-10-951-239-1	Sequence 1, Appli
13	299.6	74.0	642	13	US-11-174-398-1	Sequence 1, Appli
14	299.6	74.0	642	14	US-11-134-489-1	Sequence 1, Appli
15	298	73.6	611	16	US-11-137-807-11	Sequence 11, Appl
16	298	73.6	617	15	US-09-972-218A-18	Sequence 18, Appl
17	298	73.6	617	6	US-10-264-634-18	Sequence 18, Appl
18	298	73.6	617	8	US-10-626-169-1	Sequence 1, Appli
19	298	73.6	617	16	US-11-132-947-1	Sequence 18, Appl
20	298	73.6	399	16	US-11-197-488-18	Sequence 18, Appl
21	296.6	73.2	486	10	US-10-867-999-18	Sequence 18, Appl
22	296.6	73.2	486	9	US-09-825-561A-9	Sequence 9, Appl
23	296.6	73.2	486	9	US-10-282-622-5	Sequence 5, Appli
24	294.8	72.8	489	13	US-11-174-398-5	Sequence 5, Appli
25	294.8	72.8	486	7	US-10-282-622-3	Sequence 3, Appli
26	293.6	72.8	1560	9	US-09-923-246-3	Sequence 3, Appli
27	293.6	72.5	1560	7	US-10-295-723-84	Sequence 84, Appl
28	293.6	72.5	1560	8	US-10-659-684-84	Sequence 84, Appl
29	293.6	72.5	1560	9	US-10-787-442-84	Sequence 84, Appl
30	290.6	71.8	486	3	US-09-923-246-3	Sequence 3, Appli
31	290.6	71.8	486	7	US-10-295-723-3	Sequence 3, Appli
32	290.6	71.8	486	8	US-10-659-684-3	Sequence 3, Appli
33	290.6	71.8	486	9	US-10-787-442-3	Sequence 3, Appli
34	290.6	71.8	444	7	US-10-659-684-3	Sequence 3, Appli
35	264.4	65.3	444	13	US-11-174-398-3	Sequence 3, Appli
36	261.4	64.5	399	10	US-10-867-999-3	Sequence 3, Appli
37	259.8	64.1	399	10	US-10-867-999-13	Sequence 13, Appl
38	256	63.2	393	10	US-10-867-992-9	Sequence 9, Appli
39	256	63.2	393	10	US-10-867-992-3	Sequence 3, Appli
40	254.4	62.8	393	10	US-10-867-992-5	Sequence 5, Appli
41	254.4	62.8	393	10	US-10-867-992-1	Sequence 1, Appli
42	252.8	62.4	393	10	US-10-867-992-7	Sequence 7, Appli
43	182	44.9	3072	3	US-09-923-246-55	Sequence 55, Appl
44	182	44.9	3072	3	US-09-825-561A-46	Sequence 46, Appl
45	182	44.9	3072	7	US-10-295-723-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-09-923-246-63

Sequence 63, Application US/09923246
Patent No. US20020128446A1

GENERAL INFORMATION:
APPLICANT: NO. US20020128446A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 63
LENGTH: 483
TYPE: DNA
ORGANISM: homo sapiens
US-09-923-246-63

Query Match   74.0%;   Score 299.6;   DB 3;   Length 483;
Best Local Similarity   84.1%;
Matches 338;   Conservative   0;   Mismatches   64;   Indels   0;   Gaps   0;

Qy   4 CAAGGTCAAGATCGCGCCACACATGATTAGAAATGCCTCAACTTATTATAGATATTGTTGATCAGCTG 63
              ||||||||||||| ||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   82 CAAGGTCAAGATCGCCACACATGATTAGAAATGCGTCAACTTATTATAGATATTGTTGATCAGCTG 141

```
Qy   64  AAAAATTATGTGAATGAACTGGTTCCGGACTTCCTGCCGCTCCGGAAGATGTTGAGACC  123
         |||||||||||||||| ||| || || |  |   ||||| || |||  |  || |||| 
Db  142  AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAGAGTGTAGAGACA 201

Qy  124  AACTGTGAGTGGTCAGCTTTTTTCCTGTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA 183
         |||||||||||||| ||  ||| ||| |  ||||||| ||||||||||||||||||||| |||| 
Db  202  AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA 261

Qy  184  GGTAACAACGAAACGTTATCATCAACGTTTCATTAAAAACTGAAACGCCCAACTAAAGTCAGCAAAATACA 243
         || |||||| |||||| ||| || ||||||| |||| || |||||| |  ||| 
Db  262  GGAAACAATGAAAAGGATAATCAAATGTATCAATTAAAAAGTGAAACCACCTTCC 321

Qy  244  ACCAACGCAGGTCGTGTCGTCAGAAACAACACCGTCTGACCTGCCGCCGTCCGTGTTGATCAGCTG 303
         |||||||| | ||||  |  |||||| ||||||| | ||| |  |     | || | ||| 
Db  322  ACAAATGCAGGGAGAAGACAGAAACAACCGACTAAACATGCCCTTCATGTGACTCGTGAGGAG 381

Qy  304  AAAAAACCGCGAAAAGAATTCCTGGAAACGTTTCAAATCCTGTGAGAAATGATTCAC 363
         |||||||| | ||||||||||||| |||||||||||| |  || | |||| |||| 
Db  382  AAAAAACCACCCAAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 441

Qy  364  CAGCACCTGTCCTTCGTTACCCACCGGTTCCGAAGATTCCTGA 405
         |||| ||||||||| | ||| ||||  ||| |||||||||||| 
Db  442  CAGCATCTGTCCTTCTAGAACACACCGGAAGTGAAGAGATTCCTGA 483
```

RESULT 2
US-10-295-723-63
; Sequence 63, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens

Query Match   74.0%; Score 299.6; DB 7; Length 483;
Best Local Similarity   84.1%; Pred. No. 1.5e-87;
Matches   338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;
US-10-295-723-63

```
Qy    4  CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  63
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   82  CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 141

Qy   64  AACTGTGAGTGGTCGCGGAATTCCTGCCGGCTCCGGAAGATGTTGATCAGCTG 123
         |||||||||||||  |  || |  ||  | || |  ||||| | | ||| 
Db  142  AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAGAGTGTAGAGACA 201
```

```
Qy  124  AACTGTGAGTGGTCCGCCTTTCTCCTGTTTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
         |||||||||||||| |  ||| ||| |  ||||||  |||| |||||||||| 
Db  202  AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA 261

Qy  184  GGTAACAACGAAACGTTATCATCAACGTTTCATTAAAAACTGAAACGCCCAACTAAAGTCAGCAAAATACA 243
         || |||||| |||||| ||| || ||||||| |||| || |||||| 
Db  262  GGAAACAATGAAAAGGATAATCAAATGTATCAATTAAAAAGTGAAACCACCTTCC 321

Qy  244  ACCAACGCAGGTCGTGTCGTCAGAAACAACACCGTCTGACCTGCCGCCGTCCGTGTTGATCAGCTG 303
         |||||||| | ||||  |  |||||| ||||||| | ||| 
Db  322  ACAAATGCAGGGAGAAGACAGAAACAACCGACTAAACATGCCCTTCATGTGACTCGTGAGGAG 381

Qy  304  AAAAAACCGCGAAAAGAATTCCTGGAAACGTTTCAAATCCTGTGAGAAATGATTCAC 363
         |||||||| | ||||||||||||| |||||||||||| 
Db  382  AAAAAACCACCCAAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 441

Qy  364  CAGCACCTGTCCTTCGTTACCCACCGGTTCCGAAGATTCCTGA 405
         |||| ||||||||| | ||| ||||  ||| 
Db  442  CAGCATCTGTCCTTCTAGAACACACCGGAAGTGAAGAGATTCCTGA 483
```

RESULT 3
US-10-659-684-63
; Sequence 63, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens

Query Match   74.0%; Score 299.6; DB 8; Length 483;
Best Local Similarity   84.1%; Pred. No. 1.5e-87;
Matches   338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;
US-10-659-684-63

```
Qy    4  CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  63
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   82  CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 141

Qy   64  AACTGTGAGTGGTCAGCTTTTTTCCTGTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA 123
         |||| | | || ||  ||  | ||| |  ||||| 
Db  142  AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAGAGTGTAGAGACA 201

Qy  124  AACTGTGAGTGGTCAGCTTTTTTCCTGTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA 183
         |||||||||||||  |  ||| ||| |  ||||||| ||||||||||||||||||||| 
Db  202  AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA 261

Qy  184  GGTAACAACGAAACGTATCATCAACGTTTCATTAAAAACTGAAACGCCCAACTAAAGTCAGCAAAATACA 243
         || |||||| ||| ||| || || ||||||| 
Db  262  GGTAACAACGAAACGTATCATCAACGTTTCATTAAAAACTGAAACGCCGCTCC 243
```

RESULT 4
US-10-787-442-63
; Sequence 63, Application US/10787442
; Publication No. US20040260605A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/787,442
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-787-442-63

Query Match 74.0%; Score 299.6; DB 9; Length 483;
Best Local Similarity 84.1%; Pred. No. 1.5e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGCTCAACTTATAGATATTGTTGATCAGCTG   63
        |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   82 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  141

Qy   64 AAAAAATTATGTGAATGACCTGGTCCCGGAAATTCTGCCGGGTCCCGGAAGATGTAGAGACA  123
        |||||||||||||||||| ||||||| ||| ||||||||    ||| ||||||||||||| |
Db  142 AAAAAATTATGTGAATGACTTGGTCCCTGAAATTCTGCCCAGCTCCAGAAGATGTAGAGACA  201

Qy  124 AACTGTGAGTGGTCCGCCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAAACACC  183
        ||||||||||||||  || ||||| ||||| |||||| || |  ||||| ||||||| | |
Db  202 AACTGTGAGTGGTCAGCTTTTCTCGTTTTTCCAGAAGCGCCAACTAAAGTCAGCAAAATACA  261

Qy  184 GGTAACAACGAAGCGTATCATCAAGCGTTTCCATTAAAAAAAACTGAAGAGGAAAACACC  243
        || ||||| |||| | |||| |||| |||| ||| ||||||| | |||||||||||||| |
Db  262 GGAAACAATGAAAAGGATAATCAAATGTATCAAATTAAAAAGCTGAAGAGGAAAACCACCTTCC  321

Qy  244 ACCAACGGCAGGTCGTCGTCAGAAAACACCGTCTGACCTGCCCGTGCCTCTGTGATTCTTATGAG  303
        ||  |  | | | | |  | |||||||| |  || || ||| ||     ||  ||||||||||||
Db  322 ACAAATGCAGGGAGGAAGACAGAAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG  381

Qy  304 AAAAAACCGCCGGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC  363
        ||||||  | | |||||||||||| ||||| ||||||| | ||||| |||||||||||||
Db  382 AAAAAAACCACCCAAAAGAATTCCTAGAACACTTCAAAATCACTTCTCCAAAAAGATGATTCAT  441

Qy  364 CAGCACCTGTCCTCTCGTTACCCACCGGTTCCGAAGATTCCTGA  405
        ||||  ||||| ||  | ||| | ||| | | ||||||||||||
Db  442 CAGCCATCTGTCCCTAGAACACACCACGGAAGTGAAGAGATTCCTGA  483
```

RESULT 5
US-10-775-204-2157
; Sequence 2157, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2157
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-204-2157

Query Match 74.0%; Score 299.6; DB 10; Length 489;
Best Local Similarity 84.1%; Pred. No. 1.5e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGCTCAACTTATAGATATTGTTGATCAGCTG   63
        |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   88 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  147

Qy   64 AAAAAATTATGTGAATGACCTGGTCCCGGAAATTCTGCCGGGTCCCGGAAGATGTAGAGACC  123
        |||||||||||||||||| ||||||| ||| ||||||||    ||| ||||||||||||| |
Db  148 AAAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCCAGCTCCAGAAGATGTAGAGACA  207

Qy  124 AACTGTGAGTGGTCCGCCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAAACACC  183
        ||||||||||||||  || ||||| ||||| |||||| || |  ||||| ||||||| | |
Db  208 AACTGTGAGTGGTCAGCTTTTCTCGTTTTTCCAGAAGCGCCAACTAAAGTCAGCAAAATACA  267

Qy  184 GGTAACAACGAAGCGTATCATCAAGCGTTTCCATTAAAAAAAACTGAAGAGGAAAACACC  243
        || ||||| |||| | |||| |||| |||| ||| ||||||| | |||||||||||||| |
Db  268 GGAAACAATGAAAAGGATAATCAAATGTATCAAATTAAAAAAGCTGAAGAGGAAAACCACCTTCC  327

Qy  244 ACCAACGGCAGGTCGTCGTCAGAAAACACCGTCTGACCTGCCCGTGCCTCTGTGATTCTTATGAG  303
        ||  |  | | | | |  | |||||||| |  || || ||| ||     ||  ||||||||||||
Db  322 ACAAATGCAGGGAGGAAGACAGAAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG  381

Qy  304 AAAAAACCGCCGGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC  363
        ||||||  | | |||||||||||| ||||| ||||||| | ||||| |||||||||||||
Db  382 AAAAAAACCACCCAAAAGAATTCCTAGAACACTTCAAAATCACTTCTCCAAAAAGATGATTCAT  441

Qy  364 CAGCACCTGTCCTCTCGTTACCCACCGGTTCCGAAGATTCCTGA  405
        ||||  ||||| ||  | ||| | ||| | | ||||||||||||
Db  442 CAGCCATCTGTCCCTAGAACACACCACGGAAGTGAAGAGATTCCTGA  483
```

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAACACCGTCTGACCTGCCCGTCTTCTGTCTGATTCTTATGAG 303
         ||||| ||||| | |||||||||| |||| | | || | | | |||||||||||
Db   328 ACAAATGCAGGGAGAGACAGAAACAGAAGAAATCACTTGCTCAGGAAGAAATGAATTCTTATGAG 387

Qy   304 AAAAAAACCGCCGGAAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTCAGGAAAAATGATTCAC 363
         |||||||| ||| |||| |||||||| ||| ||||| | ||||| |||||||||||||
Db   388 AAAAAAACACCCAAAGAATTCCTAGAACACACACGGAAGTGAAGAGATTCAAAAGATGATTCAT 447

Qy   364 CAGCAACCTGTCCTTCGTACCCACGGTTCCGAAGATTCCTGA 405
         ||||| ||||||||| | |||| |||||||||
Db   448 CAGCATCTGTCCTTCTAGAACACACACGGAAGTGAAGAGATTCCTGA 489

RESULT 6
US-09-923-246-1
; Sequence 1, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: 2001-08-03
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-09-923-246-1

Query Match 74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGATCGCCACATGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
         ||||||||||||| ||||||| | ||| |||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCCGCCACTGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGACC 193

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTCGCCGGCTCCCGGAAGATGTTGAGACC 123
         |||||||||||||||||||||||||| |||||| | || | || |||||||||| |||||
Db   194 AAAAATTATGTGAATGACCTGGTTCCCGAATTTCTGCCAGTCCCAGAAGATGTAGAGACA 253

Qy   124 AACTGTGAGTGGTCCGGCTTCTCCGTGTTTCCAGAAAGCCCAACTAAAGTCAGCAAATCA 183
         ||||||||||||||| ||||| ||||||||||||| |||||||| ||| |||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTCCGTGTTTCCAGAGAGCGCCAACTAAAGTCAGCAAATACA 313

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACCGCCGTCC 243
         ||||||||||||| | ||||| ||||||||| || |||| ||||| |||||||
Db   314 GGAAACAATGAAAAGGATAATCAATGTATCAAATAAAAAGCTGAAAGAGGAAAACACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAACACCGTCTGACCTGCCCGTCTTCTGTCTGATTCTTATGAG 303
         ||||| ||||| | |||||||||| |||| | | || | | | |||||||||||
Db   374 ACAAATGCAGGGAGAGACAGAAACAGAAGAAATCACTTGCTCAGGAAGAAATGAATTCTTATGAG 433

Qy   304 AAAAAAACCGCCGGAAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTCAGGAAAAATGATTCAC 363

Qy   304 AAAAAAACCGCCGGAAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTCAGGAAAAATGATTCAC 363
         |||||||| ||| |||| |||||||| ||| ||||| | ||||| |||||||||||||
Db   434 AAAAAAACACCCAAAGAATTCCTAGAACACACACGGAAGTGAAGAGATTCAAAAGATGATTCAT 493

Qy   364 CAGCAACCTGTCCTTCGTACCCACGGTTCCGAAGATTCCTGA 405
         ||||| ||||||||| | |||| |||||||||
Db   494 CAGCATCTGTCCTTCTAGAACACACACGGAAGTGAAGAGATTCCTGA 535

RESULT 7
US-10-295-723-1
; Sequence 1, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-295-723-1

Query Match 74.0%; Score 299.6; DB 7; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGATCGCCACATGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
         ||||||||||||| ||||||| | ||| |||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGACC 193

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTCGCCGGCTCCCGGAAGATGTTGAGACA 123
         |||||||||||||||||||||||||| |||||| | || | || |||||||||| |||||
Db   194 AAAAATTATGTGAATGACCTGGTTCCCGAATTTCTGCCAGTCCCAGAAGATGTAGAGACA 253

Qy   124 AACTGTGAGTGGTCCGGCTTCTCCGTGTTTCCAGAAAGCCCAACTAAAGTCAGCAAATACA 183
         ||||||||||||||| ||||| ||||||||||||| |||||||| ||| |||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTCCGTGTTTCCAGAGAGCGCCAACTAAAGTCAGCAAATACA 313

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACCGCCGTCC 243
         ||||||||||||| | ||||| ||||||||| || |||| ||||| |||||||
Db   314 GGAAACAATGAAAAGGATAATCAATGTATCAAATAAAAAGCTGAAAGAGGAAAACACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAACACCGTCTGACCTGCCCGTCTTCTGTCTGATTCTTATGAG 303
         ||||| ||||| | |||||||||| |||| | | || | | | |||||||||||
Db   374 ACAAATGCAGGGAGAGACAGAAACAGAAGAAATCACTTGCTCAGGAAGAAATGAATTCTTATGAG 433

Qy   304 AAAAAAACCGCCGGAAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTCAGGAAAAATGATTCAC 363
         |||||||| ||| |||| |||||||| ||| ||||| | ||||| |||||||||||||
Db   304 AAAAAACCGCCGAAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTCAGGAAAAATGATTCAC 363

Left column:

```
Db    434 AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 493
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAGAGATTCCTGA 405
          ||||||||||||||||||||||||||||||||||||||||||||
Db    494 CAGCATCTGTCCTCTTAGAACACACGGAAGTGAAGATTCCTGA 535
```

RESULT 8
US-10-282-622-1

; Sequence 1, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-282-622-1

Query Match   74.0%;   Score 299.6;   DB 7; Length 642;
Best Local Similarity 84.1%;   Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy      4 CAAGGTCAAGATGCCCACATGATTAGAATGCGTCAACTTATAGATATATTGGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATATTGTTGATCAGCTG 193

Qy     64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGCGGTTCCGGAAGAATGTTGAGACC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGAGTGTAGAGACA 253

Qy    124 AACTGTGAGTGGTCCGCTTTCTCCCTGTTTCCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 AACTGTGAGTGGTCAGCTTTTTCCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA 313

Qy    184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 GGAAACAAATGAAAAGGATAAATCAAATGTATCAATTAAAAAACTGAAAGAGGAAAACCACCTTCC 373

Qy    244 ACCAACGCAGCTCGTTCGTCTGAGAAAACACCGTTCGACCTGCCGTCCGTGTTCTTATGAG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ACAAATGCAGGGAGAGACAGAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG 433

Qy    304 AAAAAACCGCGGAAAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC 363
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AAAAAACACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 493

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAGAGATTCCTGA 405
          ||||||||||||||||||||||||||||||||||||||||||||
Db    494 CAGCATCTGTCCTCTTAGAACACACGGAAGTGAAGATTCCTGA 535
```

RESULT 9
US-10-456-780-1

; Sequence 1, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.

Right column:

; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
;   TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-456-780-1

Query Match   74.0%;   Score 299.6;   DB 7; Length 642;
Best Local Similarity 84.1%;   Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy      4 CAAGGTCAAGATGCCCACATGATTAGAATGCGTCAACTTATAGATATATTGGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATATTGTTGATCAGCTG 193

Qy     64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGCGGTTCCGGAAGAATGTTGAGACC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAAGAGTGTAGAGACA 253

Qy    124 AACTGTGAGTGGTCCGCTTTCTCCCTGTTTCCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 AACTGTGAGTGGTCAGCTTTTTCCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA 313

Qy    184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 GGAAACAAATGAAAAGGATAAATCAAATGTATCAATTAAAAAACTGAAAGAGGAAAACCACCTTCC 373

Qy    244 ACCAACGCAGCTCGTTCGTCTGAGAAAACACCGTTCGACCTGCCGTCCGTGTTCTTATGAG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ACAAATGCAGGGAGAGACAGAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG 433

Qy    304 AAAAAACCGCGGAAAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC 363
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AAAAAACACCCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 493

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAGAGATTCCTGA 405
          ||||||||||||||||||||||||||||||||||||||||||||
Db    494 CAGCATCTGTCCTCTTAGAACACACGGAAGTGAAGATTCCTGA 535
```

RESULT 10
US-10-659-684-1

; Sequence 1, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547

RESULT 11
US-10-787-442-1
; Sequence 1, Application US/10787442
; Publication No. US20040260065A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/787,442
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904

; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-787-442-1

Query Match   74.0%; Score 299.6; DB 8; Length 642;
Best Local Similarity   84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAAATTATGTGAATGAACCTGGTTCCGGGAAATTCCTGCCGGCGTCCGGAAAGATGTTGAGACC 123
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAAATTATGTGAATGAACCTGGTTCCGGGAAATTCCTGCCGGCGTCCGGAAAGATGTTGAGACA 253

Qy   124 AACTGTGAGTGGTCCGGCTTTCTCCGTGTTTCCAGGAAAGCCCAGCTGAAATCCGCAAACACC 183
           ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCCAGAAGCGGCCCAACTAAAGTCAGCAAATACA 313

Qy   184 GGTAACAACGAAACGTATCATCAACGTTCCATTAAAAAACTGAAACGTAAACCGCGCGTCC 243
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAAACAATGAAACGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTTCGTCAGAAAACACCGTCTGACCTGGTCCTGTTCTTTATGAG 303
           ||||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   374 ACAAATGCAGGGAGAGGAAGACAGAAAACACAGACTAACATGGCCCTTCATGTGTTTATGAG 433

Qy   304 AAAAAAACCGCGGAAAGAAATTCCTGGAACGTTTCAAAATCCCTGCTCGCAGAAAATGATTCAC 363
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAAACCACCCAAAGAAATTCACTTCTCCAAAAGATGATTCAT 493

Qy   364 CAGCACCTGCTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
           |||||||||||||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGGAAGTGAAGAGATTCCTGA 535

RESULT 12
US-10-951-239-1
; Sequence 1, Application US/10951239
; Publication No. US20050095223A1
; GENERAL INFORMATION:
; APPLICANT: Sivakumar, Pallavur
; APPLICANT: Nelson, Andrew
; TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
; TITLE OF INVENTION: USING IL-21
; FILE REFERENCE: 03-09
; CURRENT APPLICATION NUMBER: US/10/951,239
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/505,919
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-951-239-1

Query Match   74.0%; Score 299.6; DB 10; Length 642;

; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-787-442-1

Query Match   74.0%; Score 299.6; DB 9; Length 642;
Best Local Similarity   84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAAATTATGTGAATGAACCTGGTTCCGGGAAATTCCTGCCGGCGTCCGGAAAGATGTTGAGACC 123
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAAATTATGTGAATGAACCTGGTTCCGGGAAATTCCTGCCGGCGTCCGGAAAGATGTTGAGACA 253

Qy   124 AACTGTGAGTGGTCCGGCTTTCTCCGTGTTTCCAGGAAAGCCCAGCTGAAATCCGCAAACACC 183
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCCAGAAGCGGCCCAACTAAAGTCAGCAAATACA 313

Qy   184 GGTAACAACGAAACGTATCATCAACGTTCCATTAAAAAACTGAAACGTAAACCGCGCGTCC 243
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAAACAATGAAACGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTTCGTCAGAAAACACCGTCTGACCTGGTCCTGTTCTTTATGAG 303
           ||||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   374 ACAAATGCAGGGAGAGGAAGACAGAAAACACAGACTAACATGGCCCTTCATGTGTTTATGAG 433

Qy   304 AAAAAAACCGCGGAAAGAAATTCCTGGAACGTTTCAAAATCCCTGCTCGCAGAAAATGATTCAC 363
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAAACCACCCAAAGAAATTCACTTCTCCAAAAGATGATTCAT 493

Qy   364 CAGCACCTGCTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
           |||||||||||||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGGAAGTGAAGAGATTCCTGA 535

Best Local Similarity   84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Query Match   74.0%; Score 299.6; DB 10; Length 642;

RESULT 13
US-11-174-398-1
Sequence 1, Application US/11174398
Publication No. US20050244930A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: Novak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/11/174,398
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/282,622
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(532)
US-11-174-398-1

Query Match 74.0%; Score 299.6; DB 13; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
         |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGGAATTCCTGCCGGCTCCGGAGAGATGTTGAGACC 123
         ||||||||||||||||||| ||||||||||||||||||| || |||| ||||||||||||
Db  194 AAAAATTATGTGAATGACTTGGTTCCCTGAATTTCTGCCAGCTCCAGGAGAGATGTTGAGACA 253

Qy  124 AACTGTGAGGTGGTCCGGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGAAACACC 183
         |||||||||| ||||  ||||  || |||||||||||||| |||||||||||| ||||||
Db  254 AACTGTGAGGTGGTCAGCTTTTTTCCTGTTTCCAGAAAGGGCCCAACTAAAGTCAGCAAATACA 313

Qy  184 GGTAACAACGAACGTATCATCATCAACGTTTCCATTATAAAAAACTGAAACGTAAACCGCGTCC 243
         |||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||
Db  314 GGTAACAACGAACGTATCATCATCAAACGTTTCCATTATAAAAAACTGAAACGTAAACCGCGTCC 373

Qy  244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCCGTCCTGTGATTCTTATGAG 303
         ||||||||||||||||||||||||||||||||||| ||||  |||||||||||||||||
Db  374 ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCTCCAAAAATGATTCTTATGAG 433

Qy  304 AAAAAACCGCCGAAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGAATTAC 363
         |||||| ||||||||||||||| |||||||||||||||||||||  ||||||||||||||
Db  434 AAAAAACCACCCAAAAGAATTCCTAGAAAAGATTCAAATCACTTCTCCAAAAATGATTCTTAT 493

Qy  364 CAGCACCTGCTCCTTCGTTACCCACGGTTCCGAAGAGTTCCTGA 405
         ||||||||| | |||||||||| |||||||||||||||||||||
Db  494 CAGCAATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA 535
```

RESULT 14
US-11-134-489-1
Sequence 1, Application US/11134489
Publication No. US20050265966A1
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
APPLICANT: Clegg, Christopher H.
APPLICANT: Foster, Donald C.
APPLICANT: Johnson, Rebecca A.
APPLICANT: Heipel, Mark D.
APPLICANT: ....Sivakumar, Pallavur V.
TITLE OF INVENTION: METHODS OF TREATING CANCER USING IL-21 AND MONOCLONAL ANTIBODY T[...]
FILE REFERENCE: 04-03
CURRENT APPLICATION NUMBER: US/11/134,489
CURRENT FILING DATE: 2005-05-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(532)
US-11-134-489-1

Query Match 74.0%; Score 299.6; DB 15; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
         |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGGAATTCCTGCCGGCTCCGGAGAGATGTTGAGACC 123
         ||||||||||||||||||| ||||||||||||||||||| || |||| ||||||||||||
Db  194 AAAAATTATGTGAATGACTTGGTTCCCTGAATTTCTGCCAGCTCCAGGAGAGATGTTGAGACA 253

Qy  124 AACTGTGAGGTGGTCCGGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGAAACACC 183
         |||||||||| ||||  ||||  || |||||||||||||| |||||||||||| ||||||
Db  254 AACTGTGAGGTGGTCAGCTTTTTTCCTGTTTCCAGAAAGGGCCCAACTAAAGTCAGCAAATACA 313

Qy  184 GGTAACAACGAACGTATCATCATCAACGTTTCCATTATAAAAAACTGAAACGTAAACCGCGTCC 243
         |||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||
Db  314 GGAAACAATGAAAGGATAATCAAATGTTTCCATTATCAATTAAAAGCTGAAACGTAAACCACTTCC 373

Qy  244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCCGTCCTGTGATTCTTATGAG 303
         ||||||||||||||||||||||||||||||||||| ||||  |||||||||||||||||
Db  374 ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCTCCAAAAATGATTCTTATGAG 433

Qy  304 AAAAAACCGCCGAAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAAATGATTCAC 363
         |||||| ||||||||||||||| ||||||||||||||||||| || |||||||||||||
Db  434 AAAAAACCACCCAAAAGAATTCCTAGAAAAGATTCAAATCACTTCTCCAAAAATGATTCTTATGAG 433
```

```
Db    434  AAAAAACCACCCAAAGAATTCCTAGAAGAATTCAAATCACTTCTCCAAAGATGATTCAT  493

Qy    364  CAGCACCTGTCCTCTCGTACCACCGGTTCCGAAGATTCCTGA  405
           ||||| ||| ||||| | |||| |||||||||||||||||||
Db    494  CAGCATCTGTTCCTCTAGAACACACGGAAGTGAAAGATTCCTGA  535
```

```
Query Match           73.6%;   Score 298;  DB 16;   Length 611;
Best Local Similarity  83.8%;   Pred. No. 5.7e-87;
Matches  337;  Conservative  0;  Mismatches  65;  Indels  0;  Gaps  0;

Qy      4  CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG   63
           ||||||||||||||||||||||| || ||||||| ||||||| |||| |||||||||||||
Db    128  CAAGGTCAAGAATCGGCCACATGAGTTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG  187

Qy     64  AAAAAATTATGTGAATGAACCTGGTTCCGGAAATTCCTGGCCGCCTCCGGAAGATGTTGAGACC  123
           ||| || ||| ||||| | ||| |||||| |||||||| |||||||||||||||||||||||||
Db    188  AAAAAATTATGTGAATGAACTGGTCCCTGAATTTCTGCCCAGCTCCACAGAAGATGTAGAGACA  247

Qy    124  AACTGTGAGTGGTCCGGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAACACC  183
           |||||||| ||||||  |||||| ||| |||||||||||||||||| ||||||||| |||||
Db    248  AACTGTGAGTGGTCAGCTTTTTCCTGCTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA  307

Qy    184  GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCGTCC  243
           |||||||||||||||| |||||||||| |||||||||||||| |||||||||||||||
Db    308  GGAAACAATGAAAGGAATAATCAAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC  367

Qy    244  ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCTCGTGATTCTTATGAG  303
           | ||| ||||||||| ||||| |||||| ||||||||||||||||||||||||| ||||
Db    368  ACAAATGCAGGAGAAGACAGAAAACACGACTAACACATGCCCTTCAATGTAGTTCTTATGAG  427

Qy    304  AAAAAACCGCGAAAGAATTCCTGAACGTTTCAAATCCCTGCTCGCAGAAAATGATTCAC  363
           |||||| ||||||||||| ||||||| ||||||||||||||||||||| ||||||||||
Db    428  AAAAAACCACCCAAAGAATTCCTAGAAGAATTCACTTCTCCAAAGATGATTCAT  487

Qy    364  CAGCACCTGTCCTCTCGTACCACCGGTTCCGAAGATTCCTGA  405
           |||||  |||| ||| | |||| |||||||||||||||||||
Db    488  CAGCATCTGTTCCTCTAGAACACACGGAAGTGAAAGATTCCTGA  529
```

Search completed: August 7, 2006, 12:30:07
Job time : 1012 secs

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2006 Biocceleration Ltd.

GenCore version 5.1.9

Run on: August 7, 2006, 12:24:32 ; Search time 1538 Seconds
(without alignments)
417.070 Million cell updates/sec

Title: US-10-735-149-27
Perfect score: 405
Sequence: 1 atgcaaggtcaagatcgcca..........acggttccgaagattcctga 405
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 2193277 seqs, 791917567 residues
Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Published Applications NA_New:*
1: /EMC_Celera_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celera_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celera_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celera_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celera_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celera_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celera_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celera_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celera_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celera_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	405	100.0	405	6	US-10-735-149-27	Sequence 27, Appl
c 2	299.6	74.0	642	6	US-10-511-937-565	Sequence 565, App
c 3	299.6	74.0	642	6	US-10-735-149-1	Sequence 1, Appli
c 4	299.6	74.0	642	8	US-11-266-748A-401642	Sequence 401642,
c 5	299.6	74.0	642	8	US-11-266-748A-472688	Sequence 472688,
c 6	298	73.6	617	6	US-10-806-611-1	Sequence 1, Appli
c 7	182	44.9	3072	6	US-10-806-611-3	Sequence 3, Appli
c 8	64	15.8	64	6	US-10-735-149-26	Sequence 26, Appl
c 9	63	15.6	63	6	US-10-735-149-25	Sequence 25, Appl
c 10	60	14.8	60	6	US-10-735-149-17	Sequence 17, Appl
c 11	60	14.8	60	6	US-10-735-149-18	Sequence 18, Appl
c 12	60	14.8	60	6	US-10-735-149-19	Sequence 19, Appl
c 13	60	14.8	60	6	US-10-735-149-20	Sequence 20, Appl
c 14	60	14.8	60	6	US-10-735-149-21	Sequence 21, Appl
c 15	60	14.8	60	6	US-10-735-149-22	Sequence 22, Appl
c 16	58.4	14.4	60	6	US-10-735-149-16	Sequence 16, Appl
c 17	41	10.1	50	6	US-10-735-149-15	Sequence 15, Appl
c 18	40	9.9	40	6	US-10-735-149-11	Sequence 11, Appl
c 19	40	9.9	40	6	US-10-735-149-12	Sequence 12, Appl
c 20	40	9.9	40	6	US-10-735-149-9	Sequence 9, Appli
c 21	36.8	9.1	40	6	US-10-735-149-10	Sequence 10, Appl
c 22	36.8	9.1	40	6	US-10-735-149-23	Sequence 23, Appl
c 23	32.4	8.0	26087	9	US-11-021-837-19	Sequence 19, Appl
c 24	32.2	8.0	553	8	US-11-266-748A-271776	Sequence 271776,
c 25	32.2	8.0	553	8	US-11-266-748A-332293	Sequence 332293,
c 26	32.2	8.0	724	8	US-11-266-748A-44600	Sequence 44600, A
c 27	32.2	8.0	909	8	US-11-266-748A-85263	Sequence 85263, A
c 28	32.2	8.0	909	8	US-11-266-748A-138074	Sequence 138074,
c 29	32.2	8.0	941	8	US-11-266-748A-219123	Sequence 219123,
c 30	32.2	8.0	1594	8	US-11-266-748A-242298	Sequence 242298,
c 31	32.2	8.0	2400	6	US-10-511-937-2827	Sequence 2827, Ap
c 32	32.2	8.0	6455	8	US-11-266-748A-29566	Sequence 29566, A
c 33	32	7.9	446	8	US-11-266-748A-193446	Sequence 193446,
c 34	32	7.9	446	8	US-11-266-748A-227054	Sequence 227054,
c 35	32	7.9	446	8	US-11-266-748A-241212	Sequence 241212,
c 36	32	7.9	525	8	US-11-266-748A-58700	Sequence 58700, A
c 37	32	7.9	446	8	US-11-266-748A-285687	Sequence 285687,
c 38	32	7.9	1000	8	US-11-266-748A-337116	Sequence 337116,
c 39	32	7.9	1000	8	US-11-266-748A-399967	Sequence 399967,
c 40	32	7.9	1113	8	US-11-266-748A-467013	Sequence 467013,
c 41	32	7.9	1113	8	US-11-266-748A-227053	Sequence 227053,
c 42	32	7.9	1587	8	US-11-266-748A-20672	Sequence 20672, A
c 43	32	7.9	1587	8	US-11-266-748A-62533	Sequence 62533, A
c 44	32	7.9	1587	8	US-11-266-748A-65372	Sequence 65372, A
c 45	31.2	7.7	138627	6	US-10-540-898-159	Sequence 159, App

ALIGNMENTS

RESULT 1
US-10-735-149-27

; Sequence 27, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; TITLE OF INVENTION: IN A PROKARYOTIC HOST
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 27
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: optimized IL-21
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(405)

US-10-735-149-27

Query Match   100.0%; Score 405; DB 6; Length 405;
Best Local Similarity   100.0%; Pred. No. 3.4e-127;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGCAAGGTCAAGATCGCCACATGATTAGAATGCGTCAAACTTATAGATATTGTTGATCAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCAAGGTCAAGATCGCCACATGATTAGAATGCGTCAAACTTATAGATATTGTTGATCAG 60

Qy 61 CTGAAAAATTATGTGAATGAACCTGGTTCCGGAGAATTCCTGCCGGAAGATGTTTGAG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 CTGAAAAATTATGTGAATGAACCTGGTTCCGGAGAATTCCTGCCGGAAGATGTTTGAG 120

Qy 121 ACCAACTGTGAGTGGTCCGCTTTCTCCTGTTTCCGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAAC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ACCAACTGTGAGTGGTCCGCTTTCTCCTGTTTCCGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAAC 180

Left column

```
Qy    181 ACCGGTAACAACGAACGTACATCATCAAGCGTTTCCATTAAAAAAACTGAAAACGTAAACGCCG 240
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    181 ACCGGTAACAACGAACGTATCATCAAGCGTTTCCATTAAAAAAACTGAAAACGTAAACGCCG 240

Qy    241 TCCACCAACGCCAGGTGCGTCGTTCAGAAAACACCGTCCGTCCGGAAGATGTTGATTCTTAT 300
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCCACCAACGCCAGGTCGTCGTTCAGAAAACACCGTCCGTCCGGAAGATGTTGATTCTTAT 300

Qy    301 GAGAAAAAACCCGGAAGAATTCCTGGAACGTTTCAAATCCCTGCTCGTGCAGAAAATGATT 360
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAAAAAACCCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTCGTGCAGAAAATGATT 360

Qy    361 CACCAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGAATCCTGA 405
          ||||||||||||||||||||||||||||||||||||||||||
Db    361 CACCAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGAATCCTGA 405
```

RESULT 2
US-10-511-937-565
; Sequence 565, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 565
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-565

Query Match   74.0%; Score 299.6; DB 6; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.6e-91;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy      4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy     64 AAAAAATTATGTGAATGAACTGGGTCCCTGAATTTCTGCCAGCTCCAGATGTAGAGACA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 AAAAAATTATGTGAATGAACTGGGTCCCTGAATTTCTGCCAGCTCCAGATGTAGAGACA 253

Qy    124 AACTGTGAGTGGTCCGCGTTTCTCCTGTTTCCGAAAAGCCAGCTGAAAATCCGCAAACACC 183
          |||||||||||||| ||| ||||||||||| |||||  ||   |||||||||
Db    254 AACTGTGAGTGGTCAGCTTTTCTCCTGTTTTCGAAGGCCCCAACTAAAGTCACCAAAATACA 313

Qy    184 GGTTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAACGCCGTCC 243
          || ||||  |||  || ||| |||||| ||||| |||||||   |   ||||||||||||||
Db    314 GGAAACAAATGAAAAGGATAAATCAAATGTATCAAATTAAAAAGGCTGAAGAGAGGAAACCACCTTCC 373

Qy    244 ACCAACGCCAGGTGCGTCGTTCAGAAAACACCGTCCGTCCGGAAGATGTTGATTCTTATGAG 303
          ||  |||  |||  |  |  ||| ||||| |||  |  |  |  |||||  | |||||||||
Db    374 ACAAATGCAGGGAGAGAAGACAGAAAAACAGAACTAACAACATGCCCTTCACTGTGATTCTTATGAG 433

Qy    304 AAAAAACCCGGAAGAATTCCTGGAACGTTTCAAATCCCTGCTCGTGCAGAAAATGATTCAC 363
          |||||| |||   |||||||||  | || || ||||| |  |||   |||||||||||| |
Db    434 AAAAAACACCCCAAAGAATTCCTTAGAAAGAATTCAAATCACTTCTCCAAAAGATGATTCAT 493

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGAATTCCTGA 405
          ||||| ||||||||||||||||||||||     ||||||||||||
Db    494 CAGCATCTGTCCTCTCGTACCCACGGTTGAAGAAGTGAAGAATTCCTGA 535
```

Right column

```
Qy    304 AAAAAACCCGGAAGAATTCCTGGAACGTTTCAAATCCCTGCTCGTGCAGAAAATGATTCAC 363
          |||||| |||   |||||||||  | || || ||||| |  |||   |||||||||||| |
Db    434 AAAAAACACCCCAAAGAATTCCTTAGAAAGAATTCAAATCACTTCTCCAAAAGATGATTCAT 493

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGAATTCCTGA 405
          ||||| ||||||||||||||||||||||     ||||||||||||
Db    494 CAGCATCTGTCCTCTCGTACCCACGGTTGAAGAAGTGAAGAATTCCTGA 535
```

RESULT 3
US-10-735-149-1
; Sequence 1, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; TITLE OF INVENTION: IN A PROKARYOTIC HOST
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(535)
US-10-735-149-1

Query Match   74.0%; Score 299.6; DB 6; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.6e-91;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy      4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy     64 AAAAAATTATGTGAATGAACTGGGTCCCTGAATTTCTGCCAGCTCCAGATGTAGAGACC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 AAAAAATTATGTGAATGAACTGGGTCCCTGAATTTCTGCCAGCTCCAGATGTAGAGACC 253

Qy    124 AACTGTGAGTGGTCCGCGTTTCTCCTGTTTCCGAAAAGCCAGCTGAAAATCCGCAAACACC 183
          |||||||||||||| ||| ||||||||||| |||||  || |  |||||||||
Db    254 AACTGTGAGTGGTCAGCTTTTCTCCTGTTTTCGAAGGCCCCAACTAAAGTCACCAAAATACA 313

Qy    184 GGTTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAACGCCGTCC 243
          || ||||  |||  || ||| |||||| ||||| |||||||   |   ||||||||||||||
Db    314 GGAAACAAATGAAAAGGATAAATCAAATGTATCAAATTAAAAAGGCTGAAGAGAGGAAACCACCTTCC 373

Qy    244 ACCAACGCCAGGTGCGTCGTTCAGAAAACACCGTCCGTCCGGAAGATGTTGATTCTTATGAG 303
          ||  |||  |||  |  |  ||| ||||| |||  |  |  |  |||||  | |||||||||
Db    374 ACAAATGCAGGGAGAGAAGACAGAAAAACAGAACTAACAACATGCCCTTCACTGTGATTCTTATGAG 433

Qy    304 AAAAAACCCGGAAGAATTCCTGGAACGTTTCAAATCCCTGCTCGTGCAGAAAATGATTCAC 363
          |||||| |||   |||||||||  | || || ||||| |  |||   |||||||||||| |
Db    434 AAAAAACACCCCAAAGAATTCCTTAGAAAGAATTCAAATCACTTCTCCAAAAGATGATTCAT 493

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGAATTCCTGA 405
          ||||| ||||||||||||||||||||||     ||||||||||||
Db    494 CAGCATCTGTCCTCTCGTACCCACGGTTGAAGAAGTGAAGAATTCCTGA 535
```

RESULT 4
US-11-266-748A-401642
; Sequence 401642, Application US/11266748A

; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; SOFTWARE: PatentIn version 3.3
; NUMBER OF SEQ ID NOS: 483996
;
; SEQ ID NO 401642
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-401642

Query Match   Best Local Similarity   74.0%;   Score 299.6; DB 8; Length 642;
Matches 338; Conservative 84.1%; Pred. No. 2.6e-91; Mismatches 64; Indels 0; Gaps 0;

```
Qy     4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATTATTGTTGATCAGCTG   63
         ||||||||||||| ||||||||||||||| | |||||||||||| |||||||||||||||
Db   134 CAAGGTCAAGATCGGACCCACATGATTAGAAATGGCTCAACTTATAGATAATTGTTGATCAGCTG  193

Qy    64 AAAAATTATGTGAATGAATGACCTGGTTCCCGGAATTCCTGCCGGCTCCGGAAGAGTTGAGACC  123
         |||||||||||||||||||| | ||| ||| || |||| ||| || | || |||| ||| ||
Db   194 AAAAATTATGTGAATGAATGACTTGGTCCCTGAAATTTCTGCCAGATTAGGAGATGTAGAGACA   253

Qy   124 AACTGTGAGTGGTCCCGCTTTCTCCTGTTTTCCAGAAAAGCCCAGCTGAAATCCGCAAACACC  183
         ||||||||||||| | | ||| | |||||||| |||| | ||||| | || ||| ||||| |
Db   254 AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA    313

Qy   184 GGTAACAAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAACCGCCCGTCC  243
         || ||||||| || | ||| |   ||||| ||||||||| |||||  || |  | ||| ||
Db   314 GGAAACAAATGAAAGGAGATAAATCAATTAAAAAAGCTGAAGAGAGAAAACCACCTTCC        373

Qy   244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCGTCCGTGTAGAATTTATGAG      303
         || || |||| |   | || |||||| | | | ||  ||| |  ||||| | ||||||||
Db   374 ACAAATGCAGGGAGAAGACAGAAAAACAGACTAACATCCCTTCATGTGAGTTCTTATGAG      433

Qy   304 AAAAAACCGCCGAAAAGAAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAAATGATTCAC  363
         |||||||| || ||||||| |||| | || |  ||||||   |  || || |||||||||| |
Db   434 AAAAAACCACCCAAAAGAATTCCTAGAAAATCACTTCTCCAAAAAGATGATTCAT            493

Qy   364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA                       405
         ||||| |||||||||| | ||| ||||   ||||| |||||| ||
Db   494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA                     535
```

RESULT 5
US-11-266-748A-472688
; Sequence 472688, Application US/11267748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; SOFTWARE: PatentIn version 3.3
; NUMBER OF SEQ ID NOS: 483996
;
; SEQ ID NO 472688
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-472688

Query Match   Best Local Similarity   74.0%;   Score 299.6; DB 8; Length 642;
Matches 338; Conservative 84.1%; Pred. No. 2.6e-91; Mismatches 64; Indels 0; Gaps 0;

```
Qy     4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATTATTGTTGATCAGCTG   63
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   509 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATTATTGTTGATCAGCTG   450

Qy    64 AAAAATTATGTGAATGAATGACCTGGTTCCCGGAATTCCTGCCGGCTCCGGAAGAGTTGAGACC  123
         |||||||||||||||||||| | ||| ||| || |||| ||| || | || |||| ||| ||
Db   449 AAAAATTATGTGAATGAATGACTTGGTCCCTGAAATTTCTGCCAGATTAGGAGATGTAGAGACA   390

Qy   124 AACTGTGAGTGGTCCCGCTTTCTCCTGTTTTCCAGAAAAGCCCAGCTGAAATCCGCAAACACC  183
         ||||||||||||| | | ||| | |||||||| |||| | ||||| | || ||| ||||| |
Db   389 AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA    330

Qy   184 GGTAACAAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAACCGCCCGTCC  243
         || ||||||| || | ||| |   ||||| ||||||||| |||||  || |  | ||| ||
Db   329 GGAAACAAATGAAAGGAGATAAATCAATTAAAAAAGCTGAAGAGAGAAAACCACCTTCC        270

Qy   244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCGTCCGTGTAGAATTTATGAG      303
         || || |||| |   | || |||||| | | | ||  ||| |  ||||| | ||||||||
Db   269 ACAAATGCAGGGAGAAGACAGAAAAACAGACTAACATCCCTTCATGTGAGTTCTTATGAG      210

Qy   304 AAAAAACCGCCGAAAAGAAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAAATGATTCAC  363
         |||||||| || ||||||| |||| | || |  ||||||   |  || || |||||||||| |
Db   209 AAAAAACCACCCAAAAGAATTCCTAGAAAATCACTTCTCCAAAAAGATGATTCAT            150

Qy   364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA                       405
         ||||| |||||||||| | ||| ||||   ||||| |||||| ||
Db   149 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA                     108
```

RESULT 6
US-10-806-611-1
; Sequence 1, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senices, Mayra
; APPLICANT: Young, Deborah A.

```
;  TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
;  TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
;  FILE REFERENCE: 16158-013001
;  CURRENT APPLICATION NUMBER: US/10/806,611
;  CURRENT FILING DATE: 2004-03-22
;  PRIOR APPLICATION NUMBER: US 60/456,920
;  PRIOR FILING DATE: 2003-03-21
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 1
;  LENGTH: 617
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-806-611-1

  Query Match           73.6%;  Score 298;  DB 6;  Length 617;
  Best Local Similarity 83.8%;  Pred. No. 8.9e-91;
  Matches 337;  Conservative   0;  Mismatches  65;  Indels   0;  Gaps   0;

Qy    4 CAAGGTCAAGATCGGCCACATGATTAGAATGGGTCAACTTATGATAATTGTTGATCAGCTG   63
        ||||||||||||| ||||||||||||||| ||||||||||| ||| |||||||||||||||
Db  134 CAAGGTCAAGATCCCCACATGATTAGAATCGGTCAACTTATAGATATTGTTGATCAGCTG  193

Qy   64 AAAAATTATGTGAATGAACTGGTTCCGGAAATTCCTCCGGGCTCCGGAAGATGTTGAGACC  123
        ||||| |||||||||||| ||||| || ||||||||| || |||||| |||||| ||||||
Db  194 AAAAAATTATGTGAATGACTTGGTCCCTGAATTCCTGCCAGCTCCAGAAGATGTAGAGACA  253

Qy  124 AACTGTGAGTGGGTCCGGCTTCTCTCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAAACACC  183
        ||||||||||||||| || ||||| || |||||||| ||||||| ||||| ||| ||||| ||
Db  254 AACTGTGAGTGGGTCAGCTTTTTTCCTGCTTTTCCAGAGGCCCAACTAAAGTCAGCAAATACA  313

Qy  184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC  243
        || ||||| ||| | |||||| || || ||||||||| ||||||| |||||||||| |||
Db  314 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC  373

Qy  244 ACCAACGCAGGTCGTCGTCAGAAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG  303
        || || ||||| || || |||||||||||||||||||| || |||| |||||||| |||||
Db  374 ACAAATGCAGGGAGGAGAACAGAAAACACCGTCTGACCTAACCATGCCCTTCATGTGTGATGAG  433

Qy  304 AAAAAACCCGCCGAAAGAAATTCCTGAACGTTTCAAATCCCTGCTGCCAGAAAATGATTCAC  363
        |||||||| || ||||| |||||| ||| |||||||||| | || || ||||||||||||
Db  434 AAAAAACCACCAAAGAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT  493

Qy  364 CAGCACCTGTCCTCTCGTACCACCGGTTCCGAAGATTCCTGA  405
        ||||| |||||||||| | |||| ||  | |||||||||||
Db  494 CAGCATCTGTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA  535

RESULT 7
US-10-806-611-3
;  Sequence 3, Application US/10806611
;  Publication No. US20060159655A1
;  GENERAL INFORMATION:
;  APPLICANT:  Collins, Mary
;  APPLICANT:  Chin, Elaine Y.
;  APPLICANT:  Senices, Mayra
;  APPLICANT:  Young, Deborah A.
;  TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
;  TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
;  FILE REFERENCE: 16158-013001
;  CURRENT APPLICATION NUMBER: US/10/806,611
;  CURRENT FILING DATE: 2004-03-22
;  PRIOR APPLICATION NUMBER: US 60/456,920
;  PRIOR FILING DATE: 2003-03-21
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 3
;  LENGTH: 3072
;  TYPE: DNA
;  ORGANISM: Mus musculus
US-10-806-611-3

  Query Match           44.9%;  Score 182;  DB 6;  Length 3072;
  Best Local Similarity 67.4%;  Pred. No. 5e-51;
  Matches 271;  Conservative   0;  Mismatches 130;  Indels   1;  Gaps   1;

Qy    4 CAAGGTCAAGATCGGCCACATGATTAGAATGGGTCAACTTATGATAATTGTTGATCAGCTG   63
        |||||   ||||| || ||||||||||||||    |||| ||| || ||||||| ||||||
Db  120 CAAGGGCCAGATCGCCTCCTGATTAGACCTTGCTCACCTTATTGACATTGTTGAACAGCTG  179

Qy   64 AAAAATTATGTGAATGAACTGGTTCCGGAAATTCCTCCGGGCTCCGGAAGATGTTGAGACC  123
        ||||  | ||| ||||| ||||  || || ||| | | || |||| |||||||| | |
Db  180 AAAATCTTATGAAAATGACTTGGATCCTGGATTCTTATCAGCTCCACAAGATGTAAAGGGG  239

Qy  124 AACTGTGAGTGGGTCCGGCTTCTCTCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAAACACC  183
        ||||||||| | | | |||||| | ||||||| ||| |||| |  |  || ||| |||| |
Db  240 CACTGTGAGCATGCAGCTTTTGCCTGTTTTCAGGAAGGCCAAAACTCAAGCCATCAAAACCCT  299

Qy  184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC  243
        || ||||| | |  | ||| |  || ||||| ||||||| |  |||  |||| ||| ||
Db  300 GGAAACAATAAGACATTCATCATTTGACCTCGTGGCCCAGCTCAGGAGGAGGTGCCTGCC  359

Qy  244 ACCAACGCAGGTCGTCGTCAGAAAACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG  303
        | || |  || || | | |||||| ||| | ||| || ||| ||||||||| | |||||
Db  360 AGGAGGGGAGGAGAGAAGACAGAAAGCACATAAGCTAAATCCCTTCCTGTGATTCGTATGAG  419

Qy  304 AAAAAACCCGCCGAAAGAAATTCCTGAACGTTTCAAATCCCTGCTGCCAGAAAATGATTCAC  363
        |||   || |||||| |||||| ||| |  ||||| || |   | || |||| ||||||||
Db  420 AAAAGGACACCCAAAGAATTCCTAGAAAGACTAAAAATGGGCTCCTTCAAAAGAATGATTCAT  479

Qy  364 CAGCACCTGTCCTCTCGTACCACCGGTTCCGAAGATTCCTGA  405
        ||||| || |  || ||| | |  | |  | |||||||||||
Db  480 CAGCATCTCCTTAGAACACATA-GGACCCGAAGAGATTCCTGA  520

RESULT 8
US-10-735-149-26
;  Sequence 26, Application US/10735149
;  Publication No. US20060134754A1
;  GENERAL INFORMATION:
;  APPLICANT:  Chan, Chung
;  APPLICANT:  Zamost, Bruce L.
;  APPLICANT:  Covert, Douglas C.
;  APPLICANT:  Liu, Hong Y.
;  APPLICANT:  De Jongh, Karen S.
;  APPLICANT:  Meyer, Jeffrey D.
;  APPLICANT:  Holderman, Susan D.
;  TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
;  TITLE OF INVENTION: IN A PROKARYOTIC HOST
;  FILE REFERENCE: 02-12
;  CURRENT APPLICATION NUMBER: US/10/735,149
;  CURRENT FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 26
;  LENGTH: 64
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: oligonucleotide zC40107
US-10-735-149-26

  Query Match           15.8%;  Score 64;  DB 6;  Length 64;
  Best Local Similarity 100.0%;  Pred. No. 7.2e-12;
  Matches  64;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   41 TTATAGATATTGTTGATCAGCTGAAAAATTATGTGAATGAACTGGTTCCGGAATTCCTGC  100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TTATAGATATTGTTGATCAGCTGAAAAATTATGTGAATGAACTGGTTCCGGAATTCCTGC   60

Qy  101 CGGC  104
        ||||
Db   61 CGGC   64

RESULT 9
```

```
US-10-735-149-25/c
; Sequence 25, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
;  APPLICANT: Chan, Chung
;  APPLICANT: Zamost, Bruce L.
;  APPLICANT: Covert, Douglas C.
;  APPLICANT: Liu, Hong Y.
;  APPLICANT: De Jongh, Karen S.
;  APPLICANT: Meyer, Jeffrey D.
;  APPLICANT: Holderman, Susan D.
;  TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
;  TITLE OF INVENTION: IN A PROKARYOTIC HOST
;  FILE REFERENCE: 02-12
;  CURRENT APPLICATION NUMBER: US/10/735,149
;  CURRENT FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;  LENGTH: 63
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: oligonucleotide 2C40133
US-10-735-149-25

  Query Match             15.6%;  Score 63;  DB 6;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-11;
  Matches   63;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        118 GAG 120
              |||
Db          3 GAG   1

Qy         58 CAGCTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTTCGCCGGCCTTCCGGAAGATGTT 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CAGCTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTTCGCCGGCCTTCCGGAAGATGTT   4


RESULT 10
US-10-735-149-17/c
; Sequence 17, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
;  APPLICANT: Chan, Chung
;  APPLICANT: Zamost, Bruce L.
;  APPLICANT: Covert, Douglas C.
;  APPLICANT: Liu, Hong Y.
;  APPLICANT: De Jongh, Karen S.
;  APPLICANT: Meyer, Jeffrey D.
;  APPLICANT: Holderman, Susan D.
;  TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
;  TITLE OF INVENTION: IN A PROKARYOTIC HOST
;  FILE REFERENCE: 02-12
;  CURRENT APPLICATION NUMBER: US/10/735,149
;  CURRENT FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;  LENGTH: 60
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: oligonucleotide 2C22965
US-10-735-149-17

  Query Match             14.8%;  Score 60;  DB 6;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-10;
  Matches   60;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        110 AAGATGTTGAGACCAACTGTGAGTGGTCCGGCTTTCTCCCTGTTTTCCAGAAAAGCCCAGCTGA 169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 AAGATGTTGAGACCAACTGTGAGTGGTCCGGCTTTCTCCCTGTTTTCCAGAAAAGCCCAGCTGA   1


RESULT 11
US-10-735-149-18
; Sequence 18, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
;  APPLICANT: Chan, Chung
;  APPLICANT: Zamost, Bruce L.
;  APPLICANT: Covert, Douglas C.
;  APPLICANT: Liu, Hong Y.
;  APPLICANT: De Jongh, Karen S.
;  APPLICANT: Meyer, Jeffrey D.
;  APPLICANT: Holderman, Susan D.
;  TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
;  TITLE OF INVENTION: IN A PROKARYOTIC HOST
;  FILE REFERENCE: 02-12
;  CURRENT APPLICATION NUMBER: US/10/735,149
;  CURRENT FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;  LENGTH: 60
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: oligonucleotide 2C22966
US-10-735-149-18

  Query Match             14.8%;  Score 60;  DB 6;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-10;
  Matches   60;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        150 TTTCCCAGAAAAGCCCAGCTGAAAATCCGCAAAACACCGGGTAACAACACGAAACGTTAT 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTTCCCAGAAAAGCCCAGCTGAAAATCCGCAAAACACCGGGTAACAACACGAAACGTTAT  60


RESULT 12
US-10-735-149-19/c
; Sequence 19, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
;  APPLICANT: Chan, Chung
;  APPLICANT: Zamost, Bruce L.
;  APPLICANT: Covert, Douglas C.
;  APPLICANT: Liu, Hong Y.
;  APPLICANT: De Jongh, Karen S.
;  APPLICANT: Meyer, Jeffrey D.
;  APPLICANT: Holderman, Susan D.
;  TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
;  TITLE OF INVENTION: IN A PROKARYOTIC HOST
;  FILE REFERENCE: 02-12
;  CURRENT APPLICATION NUMBER: US/10/735,149
;  CURRENT FILING DATE: 2003-12-12
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;  LENGTH: 60
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: oligonucleotide 2C22967
US-10-735-149-19

  Query Match             14.8%;  Score 60;  DB 6;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-10;
  Matches   60;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        190 AACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACCCGCCGTCCACCAAC 249
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 AACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACCCGCCGTCCACCAAC   1
```

RESULT 13
US-10-735-149-20
; Sequence 20, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; TITLE OF INVENTION: IN A PROKARYOTIC HOST
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22968
US-10-735-149-20

Query Match   14.8%; Score 60; DB 6; Length 60;
Best Local Similarity   100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   250 GCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCGTCCCGTTGATTCTTPATGAGAAAAAA 309
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCCCGTCCCGTTGATTCTTPATGAGAAAAAA 60

RESULT 14
US-10-735-149-21/c
; Sequence 21, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; TITLE OF INVENTION: IN A PROKARYOTIC HOST
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22969
US-10-735-149-21

Query Match   14.8%; Score 60; DB 6; Length 60;
Best Local Similarity   100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   290 GTGATTCTTPATGAGAAAAAAACCGCGCGAAAAGGAATTCCTGGGAACGTTTCAAATCCCTGCCTGC 349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 GTGATTCTTPATGAGAAAAAAACCGCGCGAAAAGAATTCCTGGGAACGTTTCAAATCCCTGCCTGC 1

RESULT 15
US-10-735-149-22
; Sequence 22, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; TITLE OF INVENTION: IN A PROKARYOTIC HOST
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22970
US-10-735-149-22

Query Match   14.8%; Score 60; DB 6; Length 60;
Best Local Similarity   100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   330 ACGTTTCAAATCCCTGCCTGCAGAAAAATGATTCACCAGCACCTGTCCTCTCGTTACCCACGG 389
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACGTTTCAAATCCCTGCCTGCAGAAAAATGATTCACCAGCACCTGTCCTCTCGTTACCCACGG 60

Search completed: August 7, 2006, 14:03:08
Job time : 1538 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: August 7, 2006, 12:03:42 ; Search time 2686 Seconds
                                            (without alignments)
                                            9642.109 Million cell updates/sec

Title: US-10-735-149-27
Perfect score: 405
Sequence: 1 atgcaaggtcaagatcgcca.........acggttccgaagattcctga 405

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 3197310525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	299.6	74.0	483	2	AR174605	Sequence
2	299.6	74.0	483	2	BD248998	Novel cyt
3	299.6	74.0	483	2	AR374097	Sequence
4	299.6	74.0	483	2	AR456247	Sequence
5	299.6	74.0	489	2	DD180237	Albumin F
6	299.6	74.0	564	5	BC066260	Homo sapi
7	299.6	74.0	566	5	BC066258	Homo sapi
8	299.6	74.0	566	5	BC066261	Homo sapi
9	299.6	74.0	566	5	BC066262	Homo sapi
10	299.6	74.0	642	2	AR174547	Sequence
11	299.6	74.0	642	2	BD248940	Novel cyt
12	299.6	74.0	642	2	CS034091	Sequence
13	299.6	74.0	642	2	CS036718	Sequence
14	299.6	74.0	642	2	CS043043	Sequence
15	299.6	74.0	642	2	CS045670	Sequence
16	299.6	74.0	642	2	CS080568	Sequence
17	299.6	74.0	642	2	CS237090	Sequence
18	299.6	74.0	642	2	AR374039	Sequence
19	299.6	74.0	642	2	AR456189	Sequence
20	299.6	74.0	642	5	AR705417	Sequence
21	299.6	74.0	642	5	AF254069	Homo sapi
22	298	73.6	489	2	CS135974	Sequence
23	298	73.6	566	5	BC066259	Homo sapi
24	298	73.6	611	5	BC069124	Homo sapi
25	298	73.6	617	2	DD166615	Methods a
26	296.5	73.2	486	2	AR577097	Sequence
27	296.6	73.2	486	2	AX280163	Sequence
28	294.8	72.8	489	5	AR705419	Sequence
29	293.6	72.5	1560	2	AR174624	Sequence
30	293.6	72.5	1560	2	BD249017	Novel cyt
31	293.6	72.5	1560	2	AR374116	Sequence
32	293.6	72.5	1560	2	AR456266	Sequence
33	290.6	71.8	486	2	AR174548	Sequence
34	290.6	71.8	486	2	BD248941	Novel cyt
35	290.6	71.8	486	2	AR374040	Sequence
36	290.6	71.8	486	2	AR456190	Sequence
37	264.4	65.3	444	2	AR705418	Sequence
38	232.2	57.3	459	14	AB073021	Bos tauru
39	231	57.0	2801	14	AB127975	Canis fam
40	229.4	56.6	459	14	AB073020	Sus scrof
41	184.2	45.5	441	6	AY428162	Mus muscu
42	182	44.9	3071	6	AF254070	Mus muscu
43	182	44.9	3072	2	AR174598	Sequence
44	182	44.9	3072	2	BD248991	Novel cyt
45	182	44.9	3072	2	CS080570	Sequence

ALIGNMENTS

RESULT 1
AR174605

LOCUS   AR174605   483 bp   DNA   linear   PAT 17-DEC-2001
DEFINITION Sequence 63 from patent US 6307024.
ACCESSION   AR174605
VERSION   AR174605.1   GI:17914925
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 483)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE   Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 63 23-OCT-2001;
FEATURES   Location/Qualifiers
     source   1..483
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match   74.0%; Score 299.6; DB 2; Length 483;
Best Local Similarity   84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative   0; Mismatches 64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGGCGTCAACTTATAGATAATGTTGATCAGCTG 63
              |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db   82 CAAGGTCAAGATCGCCACATGATTAGAATGGCGTCAACTTATAGATATTGTTGATCAGCTG 141

Qy   64 AAAAAATTATTGTGAATGACCTTGGTTCCCGGAAATTCCTGCGCGGAAGAATGTTGAGACC 123
              ||||||| |||||||||||||| |||||||| ||||||||||||| || | ||||||||||
Db   142 AAAAAATTATTGTGAATGACCTTGGTTCCCTGAAATTTCTGCCAGCTCCAGAGAATGAGACA 201

Qy   124 AACTGTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
              |||||||||||||||||| || ||||||||||||| |||||||||| ||| ||||| ||||
Db   202 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCCATTAAAAAAAACTGAAACGTAAACCGCCGTCC 261

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAAACTGAAACGTAAACCGCCGTCC 243
              |||| ||| |||| |||||| |||||| ||||| ||||||||||||||||||||||||||||
Db   262 GGAAACAATGAAAGGATAATCAATTGTATCAATTAAAAAAGCTGAAGAGAGAAAACCACTTCC 321

RESULT 2
LOCUS   BD248998   483 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248998
VERSION   BD248998.1 GI:33058768
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 483)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE   Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 200253839-A 59 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT   OS   Homo sapiens (human)
            PN   JP 200253839-A/59
            PD   12-NOV-2002
            PF   09-MAR-1999 JP 2000603382
            PR   09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR
            01-JUL-1999 US 60/142013
            PI   JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C PI
            FOSTER,
            PI   RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI   STACEY R DILLON,ANGELA K HAMMOND
            PC   C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
            PC   C07K14/53,
            PC   C07K14/54,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
            C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
            A61K37/02
            CC   Novel cytokine ZALPHA11 ligand
            FH   Key   Location/Qualifiers
            FT   source   1..483
            FT   /organism="Homo sapiens (human)".
FEATURES   Location/Qualifiers
     source   1..483
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   74.0%; Score 299.6; DB 2; Length 483;
Best Local Similarity   84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy    244 ACCAACGCGCAGGTCGTCGTCAGAAAACACCGTCGACCTGCCGGTCCGGTCCTGTGTGATTCTTTATGAG 303
          ||||  | | |||  | | |||||||||| || ||  ||| |  || | ||  | ||||||||||||||
Db    322 ACAAATGCAGGGAGGAGAGACAGAAACACTACACGTGCCCTTCATGTGATTCTTTATGAG 381

Qy    304 AAAAAACCGCGAAAGAATTCTTCTGCTGCAGAAATGATTCAC 363
          ||||||||  |||||||||||   |||  ||||| ||||||||
Db    382 AAAAAACCACCAAAAGAATTCCTAGAACATCACCGGAAGTGAAGATTCCTGA 441

Qy    364 CAGCACCTGTCCTCTGTACCCACCGGTTCCGGAAGATTCCTGA 405
          |||||| ||| |||| || ||| ||||  | ||||||||||||
Db    442 CAGCATCTGTTCCTCTAGAACACACCGGAAGTGAAGATTCCTGA 483
```

RESULT 3
LOCUS   AR374097   483 bp   DNA   linear   PAT 18-DEC-2003
DEFINITION Sequence 63 from patent US 6605272.
ACCESSION   AR374097
VERSION   AR374097.1 GI:40076669
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 483)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE   Methods of using zalpha11 ligand
  JOURNAL   Patent: US 6605272-A 63 12-AUG-2003;
            ZymoGenetics, Inc.; Seattle, WA
FEATURES   Location/Qualifiers
     source   1..483
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match   74.0%; Score 299.6; DB 2; Length 483;
Best Local Similarity   84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Db    202 GGTAACAAACGAAACGTATCATCAAACGTTTCATTAAAAAACTGAAAAGTAAACGGCCGTCC 261
Qy    184 GGAAACAAATGAAAAGGATAAATCAAATGTATCAAATTAAAAAGCTGAAAGAGGAAACCAACCTTCC 243
Db    262 GGAAACAAATGAAAAGGATAAATCAAATGTATCAAATTAAAAAGCTGAAAGAGGAAACCAACCTTCC 321
Qy    244 ACCAACGCAGGTCGTCGTCAGAAAACACCGTCGACCTGCCGGTCCTGTGTGATTCAGCTG 303
Db    322 ACAAATCAGGGAGAGAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTTATGAG 381
Qy    304 AAAAAACCGCCGAAAGAATTCCTGGAACGTTCAAATCGGCACACCGTCCGTC 363
Db    382 AAAAAACCACCAAAAGAATTCCTAGAACATCACCGGAAGTGAAGATTCCTGA 441
Qy    364 AACTGTGAGTGGTCGGCTATCATCAAACGTTTCATTAAAAAAACTGAAAACGCGCCGTCC 243
Db    442 CAGCACCTGTCCTCTACCCACCGGTTCCGGAAGATTCCTGA 405
```

Db   442 CAGCATCTGTCCTCTTAGAACACACGGAAGTGAAGAGATTCCTGA 483

RESULT 4
LOCUS   AR456247
DEFINITION   Sequence 63 from patent US 6686178.
ACCESSION   AR456247
VERSION   AR456247.1 GI:42691270
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown
             Unclassified.
REFERENCE   1 (bases 1 to 483)
AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
             Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
             Hammond,A.K.
TITLE   Cytokine zalpha11 ligand polynucleotides
JOURNAL   Patent: US 6686178-A 63 03-FEB-2004;
             ZymoGenetics, Inc.; Seattle, WA

FEATURES   Location/Qualifiers
     source   1..483
                     /organism="unknown"
                     /mol_type="genomic DNA"

ORIGIN

Query Match   74.0%; Score 299.6; DB 2; Length 483;
Best Local Similarity 84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 141

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAAATTCCTGCGGGTCCGGAAGATGTTGAGACC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   142 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCCTGCCAGCTCCTCAGAAGATGTAGAGACA 201

Qy   124 AACTGTGAGTGGTCACCTTTTTCCTGTTTCAGAAGAGCCCAACTAAAGTCACCAAAATACA 183
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   202 AACTGTGAGTGGTCACTTTTTCCTGTTTCAGAAGAGCCCAACTAAAGTCACCAAAATACA 261

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAACTGAAACGTAAACGCCGGTCC 243
          |||||||||||||||||||||||||||||||| || |||||||||||||||||||||
Db   262 GGAACAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGAGGAAACCACCTTCC 321

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAACACCGTCTGACCVGCCGCCTCCGTTCTTTATGAG 303
          ||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db   322 ACAAATGCAGGGAGAAGACAGAGAAACTAACAATGCCCTTCATGTGATTCTTATGAG 381

Qy   304 AAAAAAACCGCGGAAAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC 363
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   382 AAAAAAACCACCCAAAGAATTCCTAGAAGAATCAAAACACTTCTCAAAAGATGATTCAC 441

Qy   364 CAGCACCTGTCCTCTCGTGGTTCCGGAACGGGTTCCGGAAGATTCCTGA 405
          ||| || |||| |||||||||||||| ||||
Db   442 CAGCATCTGTCCTCTTAGAACACACGGAAGTGAAGAGATTCCTGA 483

REFERENCE
AUTHORS   Haseltine,W.A., Rosen,C.A., Ballance,D.J. and Turner,A.J.

TITLE   Albumin Fusion Proteins
JOURNAL   Patent: JP 2005514060-A 1222 19-MAY-2005;
             Human Genome Sciences Inc,Delta Biotechnology Limited, Principia
             Pharmaceutical Corporation
COMMENT   OS Homo sapiens
             PN JP 2005514060-A/1222
             PD 19-MAY-2005
             PF 23-DEC-2002 JP 2003560158
             PR 24-JUL-2002 US 60/398008,09-AUG-2002 US 60/402131, PR
             PR 24-OCT-2002 US 60/420246,02-OCT-2002 US 60/414984, PR
             PR 18-SEP-2002 US 60/411355,18-SEP-2002 US 60/411426, PR
             PR 13-AUG-2002 US 60/402708,11-OCT-2002 US 60/417611, PR
             PR 05-NOV-2002 US 60/423623,10-JUL-2002 US 60/394625, PR
             PR 05-JUN-2002 US 60/385708,28-MAY-2002 US 60/383123, PR
             PR 21-DEC-2001 US 60/341811,28-JAN-2002 US 60/351360, PR
             PR 08-APR-2002 US 60/370227,27-MAR-2002 US 60/367500, PR
             PR 28-FEB-2002 US 60/360000,26-FEB-2002 US 60/359370, PR
             PR 24-JAN-2002 US 60/350358,10-MAY-2002 US 60/378950, PR
             PR 24-MAY-2002 US 60/382617
             PI william a haseltine,craig a rosen,david james ballance,andrew
             PI john turner

FEATURES   Location/Qualifiers
     source   1..489
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     Key   Location/Qualifiers.

ORIGIN

Query Match   74.0%; Score 299.6; DB 2; Length 489;
Best Local Similarity 84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 147

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAAATTCCTGCGGGTCCGGAAGATGTTGAGACC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCCTGCCAGCTCCTCAGAAGATGTAGAGACA 207

Qy   124 AACTGTGAGTGGTCCGCTTTTCCTCGTTTCAGAAAGCCCAGCGTCGAAATCCGCAAACACC 183
          |||||||||||||| || ||||| |||||||||||||||||||||||||
Db   208 AACTGTGAGTGGTCAGCTTTTCCTGTTTTCAGAAGAGGCCCAACTAAAGTCAGCAAAATACA 267

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAACTGAAACGTAAACGCCGGTCC 243
          |||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db   268 GGAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGAGGAAACCACCTTCC 327

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAACACCGTCTGACCTGCCGCCTCCGTTCTTTATGAG 303
          |||||||||||||||||||||||||||||||| || |||||||||||||||||
Db   328 ACAAATGCAGGGAGAAGACAGAGAAACTAACAATGCCCTTCATGTGATTCTTATGAG 387

Qy   304 AAAAAAACCGCGGAAAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 AAAAAAACCACCCAAAGAATTCCTAGAAGAATCAAAACACTTCTCAAAAGATGATTCAT 447

Qy   364 CAGCACCTGTCCTCTCGTGGTTCCGGAACGGGTTCCGGAAGATTCCTGA 405
          ||| || |||| |||||||||||||| |||||
Db   448 CAGCATCTGTCCTCTTAGAACACACGGAAGTGAAGAGATTCCTGA 489

RESULT 6
LOCUS   BC066260
DEFINITION   Homo sapiens interleukin 21, mRNA (cDNA clone MGC:79378
             IMAGE:6971863), complete cds.
ACCESSION   BC066260
VERSION   BC066260.1 GI:42542587
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens

RESULT 5
LOCUS   DD180237   489 bp   DNA   linear   PAT 19-DEC-2005
DEFINITION   Albumin Fusion Proteins.
ACCESSION   DD180237
VERSION   DD180237.1 GI:83973219
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens

LOCUS   BC066260   564 bp   mRNA   linear   PRI 08-MAR-2005

```
REFERENCE    1 (bases 1 to 564)
AUTHORS      Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
             Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
             B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
             Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
             GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
             Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
             Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
             SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
             Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
             Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
             Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
             Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
             Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
             Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
             Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
CONSRTM      Mammalian Gene Collection Program Team
TITLE        Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED       12477932
REFERENCE    2 (bases 1 to 564)
AUTHORS      Director MGC Project.
TITLE        Direct Submission
JOURNAL      Submitted (03-FEB-2004) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
REMARK       NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Sequencing Group at the Stanford Human Genome
             Center, Stanford University School of Medicine, Stanford, CA 94305
             Web site: http://www-shgc.stanford.edu
             Contact: (Dickson, Mark) mcd@paxil.stanford.edu
             Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
             R. M.
             This clone was selected for full length sequencing because it
             passed the following selection criteria: matched mRNA gi: 11141874.

             Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRAK Plate: 172 Row: d Column: 18
FEATURES             Location/Qualifiers
     source          1..564
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79378 IMAGE:6971863"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1..564
                     /gene="IL21"
                     /note="synonyms: Za11, IL-21"
                     /db_xref="GeneID:59067"
                     /db_xref="MIM:605384"
     CDS             46..534
                     /gene="IL21"
                     /codon_start=1
                     /product="interleukin 21"
                     /protein_id="AAH66260.1"
                     /db_xref="GI:42542588"
                     /db_xref="GeneID:59067"
                     /db_xref="MIM:605384"
                     /translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLID
```

ORIGIN

```
RESULT 7
BC066258

LOCUS       BC066258               566 bp    mRNA    linear   PRI 08-MAR-2005
DEFINITION  Homo sapiens interleukin 21, mRNA (cDNA clone MGC:79376
            IMAGE:6971861), complete cds.
ACCESSION   BC066258
VERSION     BC066258.1  GI:42542658
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 566)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 566)
```

```
Query Match             74.0%;  Score 299.6; DB 5; Length 564;
Best Local Similarity   84.1%;  Pred. No. 3.8e-92;
Matches  338;  Conservative    0; Mismatches  64;  Indels    0;  Gaps    0;

Qy        4 CAAGGTCAAGATCCGCCCACATGATTAGAAATGGCTCAACTTATAGATATTGTTGATCACTG 63
            ||||||||||||||| ||||| |||||||||||||| ||||||||| ||||||||||||||||
Db      133 CAAGGTCAAGATCGCCCACATGATTAGAAATGCCTCAACTTATAGATATTGTTGATCACTG 192

Qy       64 AAAAATTATGTGAAATGACCTGGTTCCGGAAATTCCTCGCGGGCTTCCGGAAGAGATGTTGAGACC 123
            ||||| ||||||||||||||| |||||||||||| |||||||||||| ||||||||| |||||
Db      193 AAAAATTATGTGAAATGACCTGGTCCCTGAATTTCTCCGCAGCTTCCCAGAAGAGTGAGACA 252

Qy      124 AACTGTGAGTGGTCCGCGTTTCCTCGTTTTTCCAGAAAAGCCCAGCTGAAATCCGCAAACACC 183
            |||||| ||||||||||||||||||||| |||  |||||||||||||||||||||||| ||||
Db      253 AACTGTGAGTGGTCACGCTTTTTTCCGTTTTTCAGGAGGCCCAACTAAAGTCAGGCAAATACA 312

Qy      184 GGTAACAAACGAACGTATCATCAAACGTTTCATTAAAAAAACGTGAAAACGTAAACCGGCCGTCC 243
            ||| || ||||||||| |||||||||||| |||||||||||| |||||||| ||||||||||
Db      313 GGAAACAAATGAAAGGATTAATCAATTAATATCAAACAAACACCAACCTTCC 372

Qy      244 ACCAACGCAGGTCGTCCTCAGAAACACCGTCTGACCTCGCCGTCCTGTGATTCTTATGAG 303
            ||||| ||||||||||| ||||||||||||||||||||||||||||||||||| ||||||
Db      373 ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCAGTGATTCTTATGAG 432

Qy      304 AAAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGAATTCAC 363
            |||||||  || | |||||||||||||||||||||||||||||||| |||||||||||||||
Db      433 AAAAAAACCACCCAAAGAAATTCCTAGAAGAGATTCAAATCACTTCTCCAAAAAGATGATTCAT 492

Qy      364 CAGCACCTGTCCTCTCGGTACCCACCGGTTCCGGAAGATTCCTGA 405
            |||||||||||| || |||||||||| ||||||||| ||||| |||
Db      433 CAGCACCTGTCCTCTAGGTACCCACCGGTTCCGGAAGATTCCTGA 493

Qy      493 CAGCATCTTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 534
            |||||||||||||||||||||||||| |||||||||||||||||
Db      493 CAGCATCTTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 534
```

Qy: IVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKK
    LKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSILQKMIHQHLSSRTHGSE
    DS"

```
AUTHORS   Director MGC Project.
TITLE     Direct Submission
JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Narayan Bhat
          cDNA Library Preparation: Bhat Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Sequencing Group at the Stanford Human Genome
          Center, Stanford University School of Medicine, Stanford, CA 94305
          Web site: http://www-shgc.stanford.edu
          Contact: (Dickson, Mark) mcd@paxil.stanford.edu
          Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
          R. M.
          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAK Plate: 172 Row: d Column: 20
          This clone was selected for full length sequencing because it
          passed the following selection criteria: matched mRNA gi: 11141874.
FEATURES             Location/Qualifiers
     source          1..566
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79376 IMAGE:6971861"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1..566
                     /gene="Il21"
                     /note="synonyms: Zal1, IL-21"
                     /db_xref="GeneID:59067"
                     /db_xref="MIM:605384"
     CDS             46..534
                     /gene="Il21"
                     /codon_start=1
                     /product="interleukin 21"
                     /protein_id="AAH66258.1"
                     /db_xref="GI:42542659"
                     /db_xref="GeneID:59067"
                     /db_xref="MIM:605384"
                     /translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLID
                     IVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKK
                     LKRRPPSTNAGRRQKHRLTCPSCDSYEKRKPPKEFLERFKSLLQKMIHQHLSSRTHGSE
                     DS"
ORIGIN
Query Match             74.0%;  Score 299.6;  DB 5;  Length 566;
Best Local Similarity   84.4%;
Matches  338;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy        4 CAAGGTCAAGATCGCCACATGATTAGGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      133 CAAGGTCAAGATCGCCACATGATTAGGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 192

Qy       64 AAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
            |||||||||||||||||| |||||||||||||| ||||| |||||| ||||||| |||||
Db      193 AAAAAATTATGTGAATGACTTGGTTCCGGAATTTCTGCCAGCTCCAGAAGATGTAGAGACA 252

Qy      124 AACTGTGAGTGGTCAGCGTTTCTCCCGTTTCCAGAAAAGCCCAACTAAAGTCACCAAACAC 183
            ||||||||||||||| ||||| |||||||||| |     ||||||||| |||| |   ||
Db      253 AACTGTGAGTGGTCACGTTTTTCCTGTTTCCATTAAAAACTGAAAACGTAAACCGCCGGTCC 312

Qy      184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAAACGTAAACCGCCGGTCC 243
            ||  |||| ||| | ||| |||| |||||||||||||||||||||  || |||||||||||
Db      313 GGAAACAATGAAAGGATAATCAATTGTATCAATTAAAAAAGCTGAAAGAGAGAAAACCACTTCC 372

Qy      244 ACCAAACGCCAGGTGTGTCTCAGAGAACACACGTCTCGACCTGCCCGTCCTGTCGATTCTTATGAG 303
            || ||| || ||| | ||| |||| ||||||| | | ||| ||||| ||| ||| ||||||||||
Db      373 ACAAATGCAGGGGAGGAAGACAGAAACACACAGAACTAACATGCCCTTCATGTGATTCTTATGAG 432

Qy      304 AAAAAACCCCGAAAGAATTCCTGGGAACGTTTCAAATCCCGTGCTGCAGAAAATGATTCAC 363
            |||||||||   |||||||| | |||  ||||||||| |   | |||||| |||||||| |
Db      433 AAAAAACCCAACCCAAAAGAATTCTTAGAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 492

Qy      364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGAGATTCCTGA 405
            ||||| ||||||||||||||| |||   |  ||||||||||||
Db      493 CAGCATCTGTCCTCTCGTACACACACGGAAGTGAAGAGATTCCTGA 534
```

```
RESULT 8
BC066261
LOCUS       BC066261                 566 bp    mRNA    linear   PRI 08-MAR-2005
DEFINITION  Homo sapiens interleukin 21, mRNA (cDNA clone MGC:79379
            IMAGE:6971865), complete cds.
ACCESSION   BC066261
VERSION     BC066261.1  GI:42542656
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 566)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 566)
  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 11141874.
FEATURES             Location/Qualifiers
```

```
source          1..566
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="MGC:79379 IMAGE:6971865"
                /tissue_type="PCR rescued clones"
                /clone_lib="NIH MGC_195"
                /lab_host="DH10B"
                /note="Vector: pDNR-Dual"
gene            1..566
                /gene="IL21"
                /note="synonyms: Za11, IL-21"
                /db_xref="GeneID:59067"
                /db_xref="MIM:605384"
CDS             46..534
                /gene="IL21"
                /codon_start=1
                /product="interleukin 21"
                /protein_id="AAH62261.1"
                /db_xref="GI:42542617"
                /db_xref="GeneID:59067"
                /db_xref="MIM:605384"
                /translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLID
                IVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKK
                LKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSE
                DS"
ORIGIN
```

Query Match 74.0%; Score 299.6; DB 5; Length 566;
Best Local Similarity 84.1%; Pred. No. 3.8e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy    4 CAAGGTCACGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  63
        |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  133 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 192

Qy   64 AAAAATTATGTGAATGACTTGGTCCCTGAATTCTTCCCAGCTCCAGATGTAGAGACC    123
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  193 AAAAATTATGTGAATGACTTGGTCCCTGAATTCTTCCCAGCTCCAGATGTAGAGACA 252

Qy  124 AACTGTGAGTGGTCCGCTTTCTCTGTTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
        |||||||||||||| |||||| || ||||||||| |||||||  ||| ||||| ||||| |
Db  253 AACTGTGAGTGGTCAGCTTTTTCCGTTTTCAGAAGGGCCCAACTAAAGTCCAAATACA   312

Qy  184 GGTAACAACGATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCGTCC       243
        || |||||| || ||  ||| |||| || ||||| ||||| ||  ||||| ||||
Db  313 GGAAACAATGAAAGGGAATTAATCAATTATAAAAAGTGAAGAGGAAAACCACCTTCC   372

Qy  244 ACCAACGCGAGGTCGTCGTCTCAGAAAACACCGTTCTGACCTGCCGTCCTGTGAGTTCTTATGAG 303
        || ||||| ||| || ||| |||||||||||| | ||| || ||||  |  |||| | ||||||||
Db  373 ACAAATGCAGGGAGGAAGACAGAGAAAACACAGACTAACACATGCCCTTCAGTGGATTCTTATGAG 432

Qy  304 AAAAAACCGCCGAAAGAAATTCCTGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC    363
        |||||||| || |||||||||||| ||  | ||||| | |  | |||||||||||||||||
Db  433 AAAAAACCACCCAAAGAAATTCCTAGAAAGATTCAAAATCACTTCTCCAAAAGATGATTCAT    492

Qy  364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGAGATTCCTGA    405
        ||||| ||||||||| ||| | |||||  | |||||||||||||
Db  493 CAGCAATCGTCCTCTAGAACACACGGAAGTGAAAGATTCCTGA   534
```

RESULT 9

REFERENCE   1 (bases 1 to 566)
  AUTHORS   Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
            Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
            B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
            Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
            GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
            Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
            Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy
            SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
            Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
            Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
            Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
            Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
            Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
            Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
            Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
REFERENCE   2 (bases 1 to 566)
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE   Direct Submission
  JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil1.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodríguez, A., and Myers,
            R. M.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: d Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 11141874.

```
FEATURES             Location/Qualifiers
     source          1..566
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:79380 IMAGE:6971866"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
     gene            1..566
                     /gene="IL21"
                     /note="synonyms: Za11, IL-21"
                     /db_xref="GeneID:59067"
                     /db_xref="MIM:605384"
     CDS             46..534
                     /gene="IL21"
                     /codon_start=1
                     /product="interleukin 21"
                     /protein_id="AAH62262.1"
                     /db_xref="GI:42542807"
                     /db_xref="GeneID:59067"
                     /db_xref="MIM:605384"
                     /translation="MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLID
                     IVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKK
                     LKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSE
```

DS"

ORIGIN

Query Match   74.0%;   Score 299.6; DB 5; Length 566;
Best Local Similarity   84.1%;   Pred. No. 3.8e-92;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

```
Qy      4 CAAGGTCAAGATCGCCACACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG   63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 CAAGGTCAAGATCGCCACACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  192

Qy     64 AAAAATTATGTGAATGACCTGGTTCCCGGAATTCCTGCCAGCTCCAGAGAGATGTTGAGACC  123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 AAAAATTATGTGAATGACCTGGTTCCCGGAATTCCTGCCAGCTCCAGAGAGATGTTGAGACC  252

Qy    124 AACTGTGAGTGGTGGTCAGCTTTTTCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAACACC  183
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 AACTGTGAGTGGTGGTCAGCTTTTTCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA  312

Qy    184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGCGCCGTCC  243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC  372

Qy    244 ACCAACGCAGGTGCTGTTCGTCAGAAACACCGTCGACCTGACCTGCCGTCCTGTGATTCTTTATGAG  303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 ACAAATGCAGGGAAGAACGAGACAAGAAAAACACAGAGACTAACACATGCCCTTCATGTGTGATTCTTTATGAG  432

Qy    304 AAAAAACCGCCGAAAAGAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCGAGAAAATGATTGAGACC  363
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 AAAAAACCACCCAAAAGAATTCCTAGAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT  492

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA  405
          ||||||||||||||||||||||||||||||||||||||||||
Db    493 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA  534
```

RESULT 10

LOCUS   AR174547   642 bp   DNA   linear   PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6307024.
ACCESSION   AR174547
VERSION   AR174547.1 GI:17914867
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown
            Unclassified.
REFERENCE   1 (bases 1 to 642)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE   Cytokine zalpha11 ligand
  JOURNAL   Patent: US 6307024-A1 23-OCT-2001;
FEATURES   Location/Qualifiers
     source   1..642
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match   74.0%;   Score 299.6; DB 2; Length 642;
Best Local Similarity   84.1%;   Pred. No. 4e-92;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

```
Qy      4 CAAGGTCAAGATCGCCACACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG   63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  193

Qy     64 AAAAATTATGTGAATGACTTGGTCTCCCTGAATTTCTCGCCAGCTCCAGAAAAGCCTCCAAGATTAGAGACA   123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 AAAAATTATGTGAATGACTTGGTCTCCCTGAATTTCTCGCCAGCTCCAGAAAAGCCTCCAAGATTAGAGACA  253

Qy    124 AACTGTGAGTGGTGTCCCGCTTTCCTGTTTTTCAGAAAAGCCCAGCTGAAAATCGCCAAACACC  183
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 AACTGTGAGTGGTGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA  313
```

LOCUS   BD248940   642 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248940
VERSION   BD248940.1 GI:33058710
KEYWORDS   JP 2002537839-A/1.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 642)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE   Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 2002537839-A 1 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT   OS Homo sapiens (human)
            PN JP 2002537839-A/1
            PD 12-NOV-2002
            PF 09-MAR-2000 JP 2000603382
            PR 09-MAR-1999 US 09/264908,11-MAR-1999 US   09/265992 PR
            01-JUL-1999 US   60/142013
            PI JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C
            FOSTER,
            PI RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI STACEY R DILLON,ANGELA K HAMMOND
            PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,C07K14/52,
            PC C07K14/53,
            PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
            C12N1/21,
            PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
            A61K37/02
            CC Novel cytokine ZALPHA11 ligand
            FH Key   Location/Qualifiers
            FT CDS   (47)..(532).
FEATURES   Location/Qualifiers
     source   1..642
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   74.0%;   Score 299.6; DB 2; Length 642;
Best Local Similarity   84.1%;   Pred. No. 4e-92;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

```
Qy      4 CAAGGTCAAGATCGCCACACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG   63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG  193

Qy     64 AAAAATTATGTGAATGACCTGGTTCCCGGAATTCCTGCCGCGGTCCCGGAAGATGTTGAGACC  123
          |||||||||||||||||||||||||||||||||||||||
Db    194
```

RESULT 11

```
Qy    184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGCGCCGTCC  243
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC  373

Qy    244 ACCAACGCAGGTGCTGTTCGTCAGAAACACCGTCGACCTGACCTGCCGTCCTGTGATTCTTTATGAG  303
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ACAAATGCAGGGAAGAACGAGACAAGAAAAACACAGAGACTAACACATGCCCTTCATGTGTGATTCTTTATGAG  433

Qy    304 AAAAAACCGCCGAAAAGAGAATTCCTGGAACGTTTCAAAATCCCTGCTGCGAGAAAATGATTGAGACC  363
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AAAAAACCACCCAAAAGAATTCCTAGAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT  493

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA  405
          |||||||||||||||||||||||||||||||||||||
Db    494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA  535
```

```
Db   194 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGCCGGCTTCCGGGAAGATGTTGAGACA 253

Qy   124 AACTGTGAGTGGTCGGCTTTTCTCCTGTTCCTGTTTTTCCAGAAAGCCAGCTGAAATCCGCAAACACC 183

Db   254 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGAGCCCAACTAAAGTCAGCAAATACA 313

Qy   184 GGTAACAACGAAACGTATCATCAACGTTTCAATTAAAAAACTGAAACGTAAACCGCGTCC 243

Db   314 GGAAACAATGAAACGGATAATCAATGTATCAATTAAAAAGCTGAAGAGAAACCACCTTCC 373

Qy   304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363

Db   434 AAAAAACCACCCAAAGAAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAAGATGATTCAT 493

Qy   364 CAGCACCTGTTCCTCTCGTACCCACCGGTTCCGGAAGATTCCTGA 405

Db   494 CAGCATCTGTTCCTCTTAGAACACACGGAAGTGAAAGATTCCTGA 535
```

RESULT 12

```
LOCUS       CS034091                 642 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 3597 from Patent WO2005016962.
ACCESSION   CS034091
VERSION     CS034091.1  GI:60732828
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 200516962-A 3597 24-FEB-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..642
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             74.0%;  Score 299.6;  DB 2;  Length 642;
  Best Local Similarity   84.1%;  Pred. No. 4e-92;
  Matches  338;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy      4 CAAGGTCAAGATCGGCCACATGATTAGAATCGGTCAACTTATAGATATTGTTGATCAGCTG 63
Db    134 CAAGGTCAAGATCGCCACATGATTAGAATCGGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy     64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGCCGGCTTCCGGGAAGATGTTGAGACC 123
Db    194 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGCCGGCTTCCGGGAAGATGTTGAGACC 253

Qy    124 AACTGTGAGTGGTCGGCTTTTCTCCTGTTCCTGTTTTTCCAGAAAGCCAGCTGAAATCCGCAAACACC 183
Db    254 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGAGCCCAACTAAAGTCAGCAAATACA 313

Qy    184 GGTAACAACGAAACGTATCATCAACGTTTCAATTAAAAAACTGAAACGTAAACCGCGTCC 243
Db    314 GGAAACAATGAAACGGATAATCAATGTATCAATTAAAAAGCTGAAGAGAAACCACCTTCC 373

Qy    244 ACCAACGCAGGTCGTCGTCAGAAAACACCGTCGACCTGCCGCCGTCCGTCTGTGATTCTTATGAG 303
Db    374 ACAAATGCAGGGAGGAAGAGACAGACTAACATGCCCTTCATGTGATTCTTATGAG 433

Qy    304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
Db    434 AAAAAACCACCCAAAGAAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAAGATGATTCAT 493

Qy    364 CAGCACCTGTTCCTCTCGTACCCACCGGTTCCGGAAGATTCCTGA 405
Db    494 CAGCATCTGTTCCTCTTAGAACACACGGAAGTGAAAGATTCCTGA 535
```

RESULT 13

```
LOCUS       CS036718                6224 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 6224 from Patent WO2005016962.
ACCESSION   CS036718
VERSION     CS036718.1  GI:60734171
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 200516962-A 6224 24-FEB-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..642
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             74.0%;  Score 299.6;  DB 2;  Length 642;
  Best Local Similarity   84.1%;  Pred. No. 4e-92;
  Matches  338;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy      4 CAAGGTCAAGATCGGCCACATGATTAGAATCGGTCAACTTATAGATATTGTTGATCAGCTG 63
Db    134 CAAGGTCAAGATCGCCACATGATTAGAATCGGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy     64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGCCGGCTTCCGGGAAGATGTTGAGACC 123
Db    194 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGCCGGCTTCCGGGAAGATGTTGAGACC 253

Qy    124 AACTGTGAGTGGTCCCCCTTTTCTCCCTGTTTCTCCGTTTTTTCAGAAAGACCCAGCTGAAATCCGCAAACACC 183
Db    254 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGAGCCCAACTAAAGTCAGCAAATACA 313

Qy    184 GGTAACAACGAAACGTATCATCAACGTTTCAATTAAAAAACTGAAACGTAAACCGCGTCC 243
Db    314 GGAAACAATGAAACGGATAATCAATGTATCAATTAAAAAGCTGAAGAGAAACCACCTTCC 373

Qy    244 ACCAACGCAGGTCGTCGTCAGAAAACACCGTCGACCTGCCGCCGTCCGTCTGTGATTCTTATGAG 303
Db    374 ACAAATGCAGGGAGGAAGAGACAGACTAACATGCCCTTCATGTGATTCTTATGAG 433

Qy    304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
Db    434 AAAAAACCACCCAAAGAAATTCCTAGAAAGATTCAAATCACTTCTCCAAAAAGATGATTCAT 493

Qy    364 CAGCACCTGTTCCTCTCGTACCCACCGGTTCCGGAAGATTCCTGA 405
Db    494 CAGCATCTGTTCCTCTTAGAACACACGGAAGTGAAAGATTCCTGA 535
```

RESULT 14

```
LOCUS       CS043043                 642 bp    DNA     linear   PAT 22-MAR-2005
DEFINITION  Sequence 3597 from Patent WO2005019258.
ACCESSION   CS043043
VERSION     CS043043.1  GI:61850089
KEYWORDS    .
```

```
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A.; Clark,H.; Ouyang,W.; Williams,P.M.; Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 200501258-A 3597 03-MAR-2005;
            Genentech, Inc. (US)
FEATURES
     source
            1..642
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match       74.0%;   Score 299.6;  DB 2;  Length 642;
Best Local Similarity   84.1%;   Pred. No. 4e-92;
Matches   338;  Conservative    0;  Mismatches  64;  Indels    0;  Gaps    0;

Qy      4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG   63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG  193

Qy     64 AAAAAATTATTGTGAATGACCTGGTTCCGGAATTCGCCGGCTCCGGAAGATGTTGAGACC  123
          |||| ||||| |||||||||| |||| || ||||| | || || | ||||||||| ||||
Db    194 AAAAAATTATTGTGAATGACTTGGTCCCTGAATTTCTGCCAGCGTCCAGAGATGTTAGAGACA  253

Qy    124 AACTGTGAGTGGTCCGGCTTTCTCCGTTTCCAGAAAAGCCCAGCTGAAATCCGCAAACACC  183
          |||||||||||||| || ||||| ||||| ||| ||| ||||| || ||| |||||| ||
Db    254 AACTGTGAGTGGTCAGCTTTTTCCCTGTTTTTCAGGAGGCCCAACTAAAGTCAGCAAATACA  313

Qy    184 GGTAACAACGAACGTATCATCAACACGTTTCCATTAAAAAACGTAAAACCGCCGTCC  243
          || ||||| |||| |||| |||| ||| ||| | |||||||| || |||| |||| ||
Db    314 GGAAACAATGAAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGAGAAACCACCTTCC  373

Qy    244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCCTGCCCGTCGTCCTGTGATTCTTATGAG  303
          || |||| ||| | || ||||||||| | | || |||| | ||| || ||||| |||||||||
Db    374 ACAAATGCAGGGAGAGACAAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG  433

Qy    304 AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAATGATTCAC  363
          ||||||||| || |||||||||| ||| | ||||||| | || || ||||| ||||||| |
Db    434 AAAAAACCACCCAAAAGAATTCCTAGAAGAATTCAAATCACTTCTCCAAAAGATGATTCAT  493

Qy    364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA  405
          ||||| ||||||||| |||| ||||| | ||||||||||||
Db    494 CAGCAATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA  535


RESULT 15
LOCUS       CS045670
CS045670
DEFINITION  Sequence 6224 from Patent WO2005019258.
ACCESSION   CS045670
VERSION     CS045670.1  GI:61851968
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A.; Clark,H.; Ouyang,W.; Williams,P.M.; Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 200501258-A 6224 03-MAR-2005;
            Genentech, Inc. (US)
FEATURES
     source
            1..642
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"

CS045670     6224 bp     DNA     linear     PAT 22-MAR-2005
```

Search completed: August 7, 2006, 13:58:19
Job time : 2689 secs

THIS PAGE LEFT BLANK

OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

Run on: August 7, 2006, 12:03:41 ; Search time 520 Seconds
                                    (without alignments)
                                    5430.309 Million cell updates/sec

Title: US-10-735-149-27
Perfect score: 405
Sequence: 1 atgcaaggtcaagatccgcca.........acgggttccgaagattcctga 405

Scoring table: IDENTITY_NUC
               Gapop 10.0 ; Gapext 1.0
Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10499840

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_8:*
         1: geneseqn1980s:*
         2: geneseqn1990s:*
         3: geneseqn2000s:*
         4: geneseqn2001as:*
         5: geneseqn2001bs:*
         6: geneseqn2002as:*
         7: geneseqn2002bs:*
         8: geneseqn2003as:*
         9: geneseqn2003bs:*
        10: geneseqn2003cs:*
        11: geneseqn2003ds:*
        12: geneseqn2004as:*
        13: geneseqn2004bs:*
        14: geneseqn2005s:*
        15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	405	100.0	405	12	ADP70484	Adp70484 Codon opt
2	299.6	74.0	483	12	AAS20695	Aas20695 Fragment
3	299.6	74.0	483	6	ADH44633	Adh44633 Human Zal
4	299.6	74.0	483	10	ADI00969	Adi00969 Human zal
5	299.6	74.0	483	12	ADP19792	Adp19792 Human zal
6	299.6	74.0	483	14	ADV96416	Adv96416 Human zal
7	299.6	74.0	488	12	ADM41016	Adm41016 Human IL-
8	299.6	74.0	489	10	ADF17040	Adf17040 Human alb
9	299.6	74.0	489	14	ADV42801	Adv42801 Human psy
10	299.6	74.0	642	3	AAA75552	Aaa75552 DNA encod
11	299.6	74.0	642	9	AAS20637	Aas20637 cDNA enco
12	299.6	74.0	642	10	AAD47852	Aad47852 Human int
13	299.6	74.0	642	10	ADH44571	Adh44571 Human CDN
14	299.6	74.0	642	10	ADI00907	Adi00907 Immunity-
15	299.6	74.0	642	12	ADH10500	Adh10500 Human int
16	299.6	74.0	642	12	ADP10556	Adp10556 Reference
17	299.6	74.0	642	12	ADP19730	Adp19730 Human zal
18	299.6	74.0	642	12	ADP70458	Adp70458 Human int
19	299.6	74.0	642	14	ADV96354	Adv96354 Human zal
20	299.6	74.0	642	14	ADY20418	Ady20418 DNA encod
21	299.6	74.0	642	14	ADY17791	Ady17791 DNA encod
22	299.6	74.0	642	14	ADZ20500	Adz20500 cDNA enco
23	299.6	74.0	642	14	AED68670	Aed68670 Human int
24	298	73.6	489	12	ADM41018	Adm41018 Human IL-
25	298	73.6	489	14	AEB26427	Aeb26427 cDNA enco
26	298	73.6	611	15	AEE74873	Aee74873 Human IL-
27	298	73.6	617	8	ACC80873	Acc80873 Human IL-
28	298	73.6	617	12	ACD26729	Acd26729 cDNA enco
29	298	73.6	617	12	ADJ25620	Adj25620 Human int
30	298	73.6	617	13	ADS19022	Ads19022 Human int
31	298	73.6	617	15	AEE19671	Aee19671 Human int
32	298	73.6	617	15	AEG05272	Aeg05272 Human IL-
33	296.6	73.2	399	14	ADW43686	Adw43686 DNA encod
34	296.6	73.2	486	6	AAD22923	Aad22923 Human sol
35	294.8	72.8	486	9	AAD47854	Aad47854 Human int
36	293.6	72.5	486	3	AAA75599	Aaa75599 Nucleotid
37	293.6	72.5	1560	6	AAS20714	Aas20714 DNA encod
38	293.6	72.5	1560	10	ADH44654	Adh44654 Human zal
39	293.6	72.5	1560	10	ADI00990	Adi00990 MBP (malt
40	293.6	72.5	1560	12	ADP19813	Adp19813 Human zal
41	293.6	72.5	1560	14	ADV96437	Adv96437 Human zal
42	291.6	72.0	642	13	ADY27248	Ady27248 Human int
43	290.6	71.8	486	3	AAA75553	Aaa75553 Dengenera
44	290.6	71.8	486	6	AAA20638	Aaa20638 Degenerat
45	290.6	71.8	486	10	ADH44573	Adh44573 Degenerat

ALIGNMENTS

RESULT 1
ADP70484

ID   ADP70484 standard; cDNA; 405 BP.
XX
AC   ADP70484;
XX
DT   23-SEP-2004 (first entry)
XX
DE   Codon optimised interleukin 21 (IL-21) encoding cDNA SEQ ID NO:27.
XX
KW   interleukin 21; IL-21; human; gene; ss; codon optimised.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..405
FT   /*tag= a
FT   /product= "interleukin 21 (IL-21)"
XX
PN   WO2004055168-A2.
XX
PD   01-JUL-2004.
XX
PF   12-DEC-2003; 2003WO-US039764.
XX
PR   13-DEC-2002; 2002US-0433444P.
PR   13-DEC-2002; 2002US-0433452P.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Chang C, Zamost BL, Covert DC, Liu HY, De Jongh KS, Meyer JD;
PI   Holderman SD;
XX
DR   WPI; 2004-500211/47.
DR   P-PSDB; ADP70485.
XX
PT   New expression vectors for the large-scale production of IL-21 proteins
PT   comprises a prokaryotic origin of replication, a transcriptional
PT   initiation DNA element, a polynucleotide sequence and a transcriptional
PT   terminator.

```
XX
PS   Claim 1; SEQ ID NO 27; 90pp; English.
XX
CC   The present invention describes an expression vector for producing
CC   interleukin 21 (IL-21) protein. The expression vector comprises the
CC   following operably linked elements: (a) a prokaryotic origin of
CC   replication; (b) a transcriptional initiation DNA element; (c) an IL-21
CC   polynucleotide sequence having the 405 base pair sequence given in SEQ ID
CC   NO:27 (ADP70484); and (d) a transcriptional terminator. Also described:
CC   (1) a prokaryotic host cell transformed with the expression vector
CC   described above; (2) producing IL-21 proteins; (3) isolating insoluble IL
CC   -21 protein; and (4) a composition comprising an IL-21 protein comprising
CC   amino acids residues of the 134 amino acid sequence given in SEQ ID NO:28
CC   (ADP70485) at a concentration of about 10 mg/ml IL-21 protein in 10 mM
CC   histidine, and 4.7 % mannitol at pH 5.3. The composition and methods are
CC   useful for the large-scale production of IL-21 in prokaryotic hosts. The
CC   present sequence encodes a human IL-21 protein which has been codon
CC   optimised for prokaryotic expression, which is used in an example from
CC   the present invention.
XX
SQ   Sequence 405 BP; 118 A; 109 C; 83 G; 95 T; 0 U; 0 Other;

Query Match          100.0%;   Score 405;  DB 12;  Length 405;
Best Local Similarity 100.0%;
Matches  405;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1 ATGCAAGGTCAAGATCGCCACATGATTAGAAATGGTCAACTTATAGATATTGTTGATCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGCAAGGTCAAGATCGCCACATGATTAGAAATGGTCAACTTATAGATATTGTTGATCAG 60

Qy   61 CTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTGAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAG 120

Qy  121 ACCAACTGTGAGTGGTCCGCTTTCTCCGGTTTCCAGAAAGCCCAGCTGAAATCCCGAAAC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ACCAACTGTGAGTGGTCCGCTTTCTCCGGTTTCCAGAAAGCCCAGCTGAAATCCCGAAAC 180

Qy  181 ACCGGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACGCCG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ACCGGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACGCCG 240

Qy  241 TCCACCAACGCAGGTGTCGTCGTCTCAGAAAACACCGGTCCGCCCTTCCTTGATTCTTAT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCCACCAACGCAGGTGTCGTCGTCTCAGAAAACACCGGTCCGCCCTTCCTTGATTCTTAT 300

Qy  301 GAGAAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAAATCCTGCTTCAGAAAAATGATT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GAGAAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAAATCCTGCTTCAGAAAAATGATT 360

Qy  361 CACCAGCACCTGTCTCTCCGTACCCACGGTTCCGGAAGATTCCCTGA 405
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CACCAGCACCTGTCTCTCCGTACCCACGGTTCCGGAAGATTCCCTGA 405


RESULT 2
AAS20695
ID   AAS20695 standard; cDNA; 483 BP.
XX
AC   AAS20695;
XX
DT   09-APR-2002  (first entry)
XX
DE   Fragment of human zalpha11 Ligand cDNA.
XX
KW   Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW   natural killer cell proliferation; T-cell proliferation;
KW   B-cell proliferation; anti-tumour response; immune system;
KW   immunostimulant; cytostatic; human; ss.
XX
OS   Homo sapiens.
XX
PN   US6307024-B1.

XX
PD   23-OCT-2001.
XX
PF   09-MAR-2000; 2000US-00522217.
XX
PR   09-MAR-1999;  99US-0123547P.
PR   11-MAR-1999;  99US-0123904P.
PR   01-JUL-1999;  99US-0142013P.
XX
DR   WPI; 2002-040208/05.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Novak JE,  Presnell SR,  Sprecher CA,  Foster DC,  Holly RD;
PI   Gross JA,  Johnston JV,  Nelson AJ,  Dillon SR,  Hammond AK;
XX
PT   New zalpha11 ligand polypeptides and polynucleotides, useful for
PT   stimulating proliferation, activation, differentiation and/or induction
PT   of antigenic response.
XX
PS   Example 25; Col 151-152; 105pp; English.
XX
CC   The present invention relates to the isolation of a novel cytokine,
CC   zalpha11 ligand and the polynucleotide encoding it. The invention also
CC   gives the sequence for the zalpha11 receptor and the polynucleotide
CC   encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC   natural killer (NK) cells or NK cell progenitors, the activation of NK
CC   cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC   anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC   reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC   zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC   bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC   be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC   and in gene therapy. Zalpha11 Ligand may also be used to identify
CC   inhibitors of its activity, to enhance the generation of anti-tumour
CC   responses with or without the infusion of donor lymphocytes, and to
CC   activate or stimulate the immune system. The present sequence represents
CC   a fragment of human zalpha11 Ligand cDNA.
XX
SQ   Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

Query Match           74.0%;   Score 299.6;  DB 6;  Length 483;
Best Local Similarity  84.1%;
Matches  338;   Conservative   0;   Mismatches   64;   Indels   0;   Gaps   0;

Qy    4 CAAGGTCAAGATCGCCACATGATTAGAAATGGTCAACTTATAGATATTGTTGATCAGCTG 63
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 CAAGGTCAAGATCGCCACATGATTAGAAATGGGTCAACTTATAGATATTGTTGATCAGCTG 141

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGATGTTGAGACC 123
        ||||||||||||||||||| ||| || ||||| | || |  |  ||||||||||| || |
Db  142 AAAAATTATGTGAATGACTTGGTCCCTGAATTCTCGCCAGTCTCCAGAAGATGTTAGACA 201

Qy  124 AACTGTGAGTGGTCCGCTTTCTCCGTTTTCCGTTTTCAGAAAGGCCCAACTAAAGTCAGC 183
        |||||||||||||| ||||| || || ||||||| ||||||  ||||| || || | | |
Db  202 AACTGTGAGTGGTCAGCTTTTTCCCTGTTTTCAGAAGAGGCCCAACTAAAGTCAGCAAATACA 261

Qy  184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACGCCGTCC 243
        || ||||| | |  ||||||||| || |||| |||||||| |||||   |  |  | ||
Db  262 GGAAACAAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGACACACTTCC 321

Qy  244 ACCAACGCAGGTGTCGTCGTCTCAGAAAACACCGGTCCGCCCTTCCTTGATTCTTATGAG 303
        ||  | ||||| |  || | |  ||||||| || || |  |||||| |||||||||||||
Db  322 ACAAATGCAGGGAAGAAGAGAAACACAGAGTAACATGCCCTTCAATCTGATTCTTATGAG 381

Qy  304 AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCTGCTTCAGAAAAATGATTCAC 363
        |||||||| || |||  ||||||| | |   | ||| | |||  ||||| ||||||||
Db  382 AAAAAACCACCCAAAAGAATTCCTTAGAAAGAAATCACTTCTCCAAAAGAATGATTCAT 441

Qy  364 CAGCACCTGTCTCTCCGTACCCACGGTTCCGGAAGATTCCCTGA 405
        |||||||||||  ||  | ||  ||||   |  | |||||||||
Db  442 CAGCACCTGTCCTCTAGAACACACCGGAGGTGAAGTGAAGATTCCCTGA 483
```

RESULT 3
ADH44633
ID   ADH44633 standard; DNA; 483 BP.
XX
AC   ADH44633;
XX
DT   25-MAR-2004 (first entry)
XX
DE   Human Zalpha11 ligand cDNA fragment.
XX
KW   Human; ss; Zalpha11 ligand; zalpha11 receptor; immune response;
KW   tumour progression; metastasis; tumour stasis; haematopoietic tumour;
KW   lymphoma; B cell tumour; systemic lupus erythematosus;
KW   rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
KW   immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
XX
OS   Homo sapiens.
XX
PN   US6050272-B2.
XX
PD   12-AUG-2003.
XX
PF   03-AUG-2001; 2001US-00923246.
XX
PR   09-MAR-1999; 99US-01235547P.
PR   11-MAR-1999; 99US-0123904P.
PR   01-JUL-1999; 99US-0142013P.
PR   09-MAR-2000; 2000US-00522217.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Novak JE,   Presnell SR,   Sprecher CA,   Foster DC,   Holly RD;
PI   Gross JA,   Johnston JV,   Nelson AJ,   Dillon SR,   Hammond AK;
XX
DR   WPI; 2003-895283/82.
XX
PT   Stimulating an immune response in a mammal exposed to an antigen or
PT   pathogen, useful for enhancing anti-tumor activity resulting in reduced
PT   tumor progression or metastasis, comprises administering zalpha11 ligand
PT   polypeptide.
XX
PS   Example 25; SEQ ID NO 63; 103pp; English.
XX
CC   The invention relates to stimulating an immune response in a mammal
CC   exposed to an antigen or pathogen comprises administering a composition
CC   comprising mature zalpha11 ligand polypeptide comprising residues 32-162
CC   of ADH4572 in a pharmaceutical vehicle. Also included are stimulating an
CC   immune response in a mammal exposed to an antigen or pathogen
CC   (comprising: (a) determining the level of antigen or
CC   pathogen present in the mammal; (b) directly the level of
CC   comprising zalpha11 ligand polypeptide in a pharmaceutical vehicle; (c)
CC   determining (in)directly the level of antigen or pathogen in the mammal;
CC   and (d) comparing the antigen or pathogen level in (a) with (b), where a
CC   change in the level indicates stimulation of immune response), and
CC   stimulating an immune response in a mammal exposed to an antigen or
CC   pathogen (comprising: (a) determining a level of antigen- or pathogen-
CC   specific antibody; (b) administering a composition comprising zalpha11
CC   ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
CC   administration level of the antigen- or pathogen-specific antibody; and
CC   (d) comparing the level of the antibody in (a) with (b), where an
CC   increase in the antibody level indicates stimulation of immune response).
CC   The method is useful for stimulating an immune response in a mammal
CC   exposed to an antigen or pathogen, and for enhancing anti-tumour activity
CC   resulting in a reduction in tumour progression, decrease in metastasis,
CC   or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
CC   or a B cell tumour. The zalpha11 ligand is useful for treating a wide
CC   range of diseases arising from defects in the immune system, e.g.
CC   systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
CC   diabetes, for boosting immunity to infectious diseases, treating
CC   immunocompromised patients, such as HIV+ patients and in improving
CC   vaccines. The present sequence is a human zalpha11 ligand cDNA (or

---

CC   fragment).
XX
SQ   Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

Query Match   74.0%; Score 299.6; DB 10; Length 483;
Best Local Similarity 84.1%; Pred. No. 1.3e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy   4 CAAGGTCAAGATCGCCCACATGATTAGAATGCGTCAACTTTATAGATATTGTTGATCAGCTG 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 CAAGGTCAAGATCGCCCACATGATTAGAATGCGTCAACTTTATAGATATTGTTGATCAGCTG 141

Qy   64 AAAAAATTATGTGAATGAACCTGGTTCCGGAATTCCTGCGCGGCTCCCGGAAGATTGTGAGACC 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   142 AAAAAATTATGTGAATGAACCTGGTTCCGGAATTCCTGCGCGGCTCCCGGAAGATTGTGAGACA 201

Qy   124 AACTGTGAGTGGTGGTCCGCCTTCTCCTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202 AACTGTGAGTGGTGGTCAGCTTTTTCCTGTTTTCCAGAAGGCCCAACTAAAGTCAGCAAATACA 261

Qy   184 GGTAACACGAACGTATCATCAACGTTTCCATTAAAAAACGTAAAACGTGTCC 243
              ||||||||||||||||||||||||||||||||||||||||||||
Db   262 GGAAACAATGAAAGACGATAATCAATGTATCAAATTAAAAAACGTGAAGAGGAAACCACCTTCC 321

Qy   244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCTGACCTGCCGTCCTGTGATTCTTATGAG 303
              ||||||||||||||||||||||||||||||||||||||
Db   322 ACAAATGCAGGGGAGGAAGACAGAGAAACACAGATAACATGCCCTTCATGTGATTCTTATGAG 381

Qy   304 AAAAAAACCGCCGAAAAGAATTCCCTGGAAACGTTTCAAATCCCTGCTGCGAGAAAAATGATTCAC 363
              ||||||||||||||||||||||||||||||||||||||||||||||
Db   382 AAAAAAACCACCCAAAAGAATTCCTAGAAAAGAATTCAAATCACTCTTCCAAAAAGATGATTCAT 441

Qy   364 CAGGACACCTGTCCTCGTACCCACGGGTTCCGGAAGATTCCTGA 405
              ||||||||||||||||||||||||||||||||||
Db   442 CAGCATCCTGTCCCTAGAAACACACGGAAGTGAAGAGATTCCTGA 483

RESULT 4
ADI00969
ID   ADI00969 standard; cDNA; 483 BP.
XX
AC   ADI00969;
XX
DT   22-APR-2004 (first entry)
XX
DE   Human zalpha11 ligand cDNA fragment - SEQ ID 63.
XX
KW   zalpha11 ligand; immunity; infectious disease; immunocompromised patient;
KW   HIV; vaccine; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2003125524-A1.
XX
PD   03-JUL-2003.
XX
PF   15-NOV-2002; 2002US-00295723.
XX
PR   09-MAR-2000; 2000US-00522217.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Novak JE,   Presnell SR,   Sprecher CA,   Foster DC,   Holly RD;
PI   Gross JA,   Johnston JV,   Nelson AJ,   Dillon SR,   Hammond AK;
XX
DR   WPI; 2003-811003/76.
XX
PT   New zalpha11 ligand polypeptides, useful for boosting immunity to
PT   infectious diseases, and treating immunocompromised patients, such as
PT   human immunodeficiency virus (HIV) patients, or in improving vaccines.
XX
PS   Example 25; SEQ ID NO 63; 113pp; English.
XX

RESULT 5
ADP19792

ID   ADP19792 standard; DNA; 483 BP.
XX
AC   ADP19792;
XX
DT   26-AUG-2004 (first entry)
XX
DE   Human zalpha11 ligand fragment seqid 63.
XX
KW   cytostatic; zalpha11 ligand; pharmaceutical; cancer; immune response;
KW   melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   US2004110932-A1.
XX
PD   10-JUN-2004.
XX
PF   10-SEP-2003; 2003US-0059684.
XX
PR   09-MAR-1999; 99US-0123547P.
PR   11-MAR-1999; 99US-0123904P.
PR   01-JUL-1999; 99US-0142013P.
PR   09-MAR-2000; 2000US-0522217.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI   Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
CC   The invention relates to a novel isolated zalpha11 ligand polypeptide.
CC   The polypeptide of the invention may be useful for boosting immunity to
CC   infectious diseases and treating immunocompromised patients, such as HIV
CC   patients, as well as in improving vaccines. The current sequence is that
CC   of the human zalpha11 ligand cDNA fragment of the invention.
XX
SQ   Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

Query Match   74.0%; Score 299.6; DB 10; Length 483;
Best Local Similarity   84.1%; Pred. No. 1.3e-83;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 CAAGGTCAAGATCCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 141

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGGCTTCCGGAAGATGTTGAGACC 123
              |||||||||||||||||| ||| || || ||||||||| |||||| |||||||||| |||
Db   142 AAAAATTATGTGAATGACTTGGTCCCTGAATTCCTGCCAGCTTCCAGAAGATGTTAGAGACA 201

Qy   124 AACTGTGAGTGGTCAGCTTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAACACC 183
              ||||||||||||||||||||| |||||||| |||||||||||| | |||| ||| ||| ||
Db   202 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAAGCCCAACTAAAGTCAGCAAATACA 261

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAACCGCGTCC 243
              || ||||| ||| || | || || || ||||||| | ||||| || ||| ||| ||
Db   262 GGAAACAATGAAAAGGATTAATCAATTAAAAAGCTTGAAGAGGAAAACCACCTTCC 321

Qy   244 ACCAACGCAGGTCGTCGTCAGAAAACACCGGTCTGACCTGCCCGTCGTTGATTCTTATGAG 303
              |||||| ||| | | ||||| ||| || || ||||||||| | |||||||||||||||
Db   322 ACAAATGCAGGGAGGAAGACAGAAAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG 381

Qy   304 AAAAAACCCGCGAAAGAATTCCTGCTCGAACGTTTCAAATCCCTGCTTCAGAAAATGATTCAC 363
              |||||||| | ||||||||||| | ||| ||||||||| || |||| ||| |||||||| |
Db   382 AAAAAACCACCCAAAGAATTCCTAGAAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 441

Qy   364 CAGCACCTGTCCTCTGTACCCACGGTTCCGGAAGAGTTCCTGA 405
              ||||| |||||||| | | |||| || |||| ||||||||
Db   442 CAGCATCTGTCCTCTAGAACACACCGGAAGTGAAGAGATTCCTGA 483

RESULT 6
ADV96416

ID   ADV96416 standard; cDNA; 483 BP.
XX
AC   ADV96416;
XX
DT   10-MAR-2005 (first entry)
XX
DR   WPI; 2004-440401/41.
XX
PT   New zalpha11 ligand polynucleotide and polypeptide molecules, useful for
PT   treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or
PT   lymphoma.
XX
PS   Example 25; SEQ ID NO 63; 111pp; English.
XX
CC   The invention describes an isolated polynucleotide comprising a sequence of
CC   amino acid residues that is at least 90 or 95% identical to residues 41
CC   (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino
CC   acids (SEQ ID NO:2, human zalpha11 ligand), fully defined in the
CC   specification. Also described are: a pharmaceutical composition
CC   comprising the polypeptide, and a vehicle; a method of treating cancer in
CC   a mammal; a method of stimulating an immune response in a mammal with
CC   melanoma; a method of stimulating an immune response in a mammal bearing
CC   a tumour; an isolated polynucleotide comprising a sequence of nucleotides
CC   that encode amino acid residues cited above, where the polynucleotide
CC   encodes a polypeptide that binds a receptor comprising 538 amino acids,
CC   fully defined in the specification; a pharmaceutical composition
CC   comprising the polynucleotide encoding, in a pharmaceutically acceptable
CC   vehicle; an expression vector comprising the following operably linked
CC   elements; a control element; and a DNA segment comprising the
CC   polynucleotide; and an isolated polynucleotide molecule comprising at
CC   least 10 nucleotides of the polynucleotide sequence of 642 bp, fully
CC   defined in the specification. The molecules, compositions and methods are
CC   useful for treating cancer, e.g. melanoma, solid tumour, haematopoietic
CC   tumour, or lymphoma. This sequence represents a human zalpha11 ligand
CC   polynucleotide used in the creation of a zalpha11 ligand expression
CC   vector.
XX
SQ   Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

Query Match   74.0%; Score 299.6; DB 12; Length 483;
Best Local Similarity   84.1%; Pred. No. 1.3e-83;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 CAAGGTCAAGATCCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 141

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGGCTTCCGGAAGATGTTGAGACC 123
              |||||||||||||||||| ||| || || ||||||||| |||||| |||||||||| |||
Db   142 AAAAATTATGTGAATGACTTGGTCCCTGAATTCCTGCCAGCTTCCAGAAGATGTTAGAGACA 201

Qy   124 AACTGTGAGTGGTCAGCTTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAACACC 183
              ||||||||||||||||||||| |||||||| |||||||||||| | |||| ||| ||| ||
Db   202 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAAAGCCCAACTAAAGTCAGCAAATACA 261

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAACCGCGTCC 243
              || ||||| ||| || | || || || ||||||| | ||||| || ||| ||| ||
Db   262 GGAAACAATGAAAAGGATTAATCAATTAAAAAGCTTGAAGAGGAAAACCACCTTCC 321

Qy   244 ACCAACGCAGGTCGTCGTCAGAAAACACCGGTCTGACCTGCCCGTCGTTGATTCTTATGAG 303
              |||||| ||| | | ||||| ||| || || ||||||||| | |||||||||||||||
Db   322 ACAAATGCAGGGAGGAAGACAGAAAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG 381

Qy   304 AAAAAACCCGCGAAAGAATTCCTGCTCGAACGTTTCAAATCCCTGCTTCAGAAAATGATTCAC 363
              |||||||| | ||||||||||| | ||| ||||||||| || |||| ||| |||||||| |
Db   382 AAAAAACCACCCAAAGAATTCCTAGAAAAGATTCAAATCACTTCTCCAAAAGATGATTCAT 441

Qy   364 CAGCACCTGTCCTCTGTACCCACGGTTCCGGAAGAGTTCCTGA 405
              ||||| |||||||| | | |||| || |||| ||||||||
Db   442 CAGCATCTGTCCTCTAGAACACACCGGAAGTGAAGAGATTCCTGA 483

```
XX
DE   Human zalpha11 ligand cDNA sequence - SEQ ID 63.
XX
KW   stem cell; cell culture; zalpha11 ligand; ss.
XX
OS   Homo sapiens.
XX
PN   US20042260065-A1.
XX
PD   23-DEC-2004.
XX
PF   26-FEB-2004; 2004US-00787442.
XX
PR   09-MAR-1999;   99US-0123547P.
PR   11-MAR-1999;   99US-0123904P.
PR   01-JUL-1999;   99US-0142013P.
PR   09-MAR-2000;   2000US-00522217.
XX
DR   WPI; 2005-038783/04.
XX
PI   Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI   Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
PA   (NOVA/) NOVAK J E.
PA   (PRES/) PRESNELL S R.
PA   (SPRE/) SPRECHER C A.
PA   (FOST/) FOSTER D C.
PA   (HOLL/) HOLLY R D.
PA   (GROS/) GROSS J A.
PA   (JOHN/) JOHNSTON J V.
PA   (NELS/) NELSON A J.
PA   (DILL/) DILLON S R.
PA   (HAMM/) HAMMOND A K.
XX
PS   Example 25; SEQ ID NO 63; 110pp; English.
XX
PT   New zalpha 11 ligand fusion protein, useful for stimulating the
PT   proliferation and/or development of hematopoietic cells in vitro and in
PT   vivo, and in autologous marrow culture.
XX
CC   The invention comprises a fusion protein that contains a zalpha11 ligand
CC   and a cytokine polypeptide (e.g. IL-2, IL-4, IL-15 or GM-CSF), the fusion
CC   protein of the invention binds to the human receptor protein. The fusion
CC   protein of the invention is useful for stimulating the proliferation and/or
CC   development of hematopoietic cells. The protein of the invention is also
CC   useful in autologous marrow culture. The present cDNA sequence represents
CC   a fragment of the human zalpha11 ligand coding sequence.
XX
SQ   Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

Query Match        74.0%;  Score 299.6;  DB 14;  Length 483;
Best Local Similarity   84.1%;  Pred. No. 1.3e-83;
Matches  338;  Conservative   0;  Mismatches   64;  Indels   0;  Gaps   0;

Qy     4 CAAGGTCAAGATCGCCACATGATTAGGAATGGTCAACTTATAGATATTGTTGATCAGCTG 63
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    82 CAAGGTCAAGATCGCCACATGATTAGTTCAACTTATAGATATTGTTGATCAGCTG 141

Qy    64 AAAAAATTATGTGAATGAATGACCTGGTTCCCGTTCCCTGAATTTCTGCCAGAAGCCCAC 123
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   142 AAAAAATTATGTGAATGAATGACCTGGTTCCCTGCCTCCAGAAGATGTTAGAGACA 201

Qy   124 AACTGTGAGTGGTCCGGCTTTCTCCCGTTCCAGAAGACCCACTGAAAATCCCAAACACC 183
         ||||||||||||||||| ||||||| ||||| |||||| |||||| |||||| ||||||
Db   202 AACTGTGAGTGGTCACGCTTTTTCCTGTTTTCAGAAGAGCCCACTAAAGTCAGCAAAATACA 261

Qy   184 GGTAACAACGAGCGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACCGCCGTCC 243
         || |||||||| |||| | ||||| |||| ||||||| |||||||| |||| ||||||||
Db   262 GGAAACAACGAAAGGATAAATCAAATGTATCATCAAATTAAAAAGCTGAAAGAAAACCACCTTCC 321

Qy   244 ACCAAGGCACAGTGTTCGTTGTTCAGAAAACACCGTCTTGACCTGCCCGTCCCTTCATGTGTCTTATGAG 303
         || ||| ||||| |||||| ||| ||||||||| |||||| | |||||||| ||||| ||||||
Db   322 ACAAATCCAGGGAGAAGAGAACAGAAAACACTAACATGCCCTTCATGTGATTCTTATGAG 381
```

```
Qy   304 AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTGCAGAAAAATGATTCAC 363
         |||||||| || ||||||||||| |||| | ||||| || || | |||| |||||||||
Db   382 AAAAAACCACCCAAAGAATTCCTAGAAGACAGATTCAAATCACTTCTCCAAAAGATGATTCAT 441

Qy   364 CAGCACCTGTCCCTCGTACCCAGGGTTCCGAGAGATTCCTGA 405
         ||||| |||||| || | || |  |||| || ||||||||||
Db   442 CAGCATCTGTCCTCTAGACACACACGGAAGTGAAGAGATTCCTGA 483


RESULT 7
ADM41016
ID   ADM41016 standard; DNA; 488 BP.
XX
AC   ADM41016;
XX
DT   15-JUL-2004 (first entry)
XX
DE   Human IL-21 encoding DNA, seq id 1.
XX
KW   Antiallergic; antiasthmatic; antiparasitic; antiinflammatory;
KW   anthelmintic; dermatological; immunomodulator; interleukin; IL-21;
KW   eosinophil; allergic; parasitic; asthma; allergic rhinitis;
KW   helminthic infection; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200432953-A1.
XX
PD   22-APR-2004.
XX
PF   13-OCT-2003; 2003WO-DK000691.
XX
PR   11-OCT-2002; 2002DK-00001546.
PR   16-OCT-2002; 2002DK-00001587.
PR   17-OCT-2002; 2002US-0419225P.
XX
DR   WPI; 2004-340821/31.
XX
PI   Romer J, Moller NPH, Skak K;
XX
PA   (NOVO ) NOVO NORDISK AS.
XX
PS   Disclosure; SEQ ID NO 1; 32pp; English.
XX
PT   Use of Interleukin-21 for the treatment of diseases or conditions where
PT   eosinophils are involved in a protective response in a subject, e.g.
PT   allergic conditions and/or parasitic diseases.
XX
CC   The invention relates to an interleukin (IL)-21 that is used for the
CC   treatment of diseases or conditions where eosinophils are involved in a
CC   protective response in a subject, e.g. allergic conditions and/or
CC   parasitic diseases. Methods of the invention are useful for the treatment
CC   of diseases or conditions where eosinophils are involved in a protective
CC   response in a subject, such as allergic conditions (e.g. asthma, allergic
CC   rhinitis or allergic diseases of the skin) and/or parasitic diseases,
CC   especially helminthic infection. The current sequence represents the DNA
CC   sequence encoding IL-21. Note: This sequence does not decode to that of
CC   ADM41017, which we are told in the specification is the amino acid
CC   sequence of IL-21.
XX
SQ   Sequence 488 BP; 170 A; 103 C; 98 G; 117 T; 0 U; 0 Other;

Query Match        74.0%;  Score 299.6;  DB 12;  Length 488;
Best Local Similarity   84.1%;  Pred. No. 1.3e-83;
Matches  338;  Conservative   0;  Mismatches   64;  Indels   0;  Gaps   0;

Qy     4 CAAGGTCAAGATCGCCACATGATTAGGAATGGTCAACTTATAGATATTGTTGATCAGCTG 63
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    87 CAAGGTCAAGATCGCCACATGATTAGTTCAACTTATAGATATTGTTGATCAGCTG 146

Qy    64 AAAAAATTATGTGAATGAATGACCTGGTTCCGGAATTCCTGCCCGGCTCCGGAAGAATGTTGAGACC 123
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       AAAAAATTATGTGAATGAATGACCTGGTTCCGGAATTCCTGCCCGGCTCCGGAAGAATGTTGAGACC
```

```
RESULT 8

ID   ADF17040 standard; DNA; 489 BP.
XX
AC   ADF17040;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human albumin fusion protein-related DNA sequence SeqID2157.
XX
KW   albumin fusion protein; human serum albumin;
KW   serum osmotic pressure; shelf-life; stability; antidiabetic;
KW   gene therapy; diabetes mellitus; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003060071-A2.
XX
PD   24-JUL-2003.
XX
PF   23-DEC-2002;  2002WO-US040891.
XX
PR   21-DEC-2001;  2001US-0341811P.
PR   24-JAN-2002;  2002US-0350358P.
PR   28-JAN-2002;  2002US-0351360P.
PR   26-FEB-2002;  2002US-0359370P.
PR   28-FEB-2002;  2002US-0360000P.
PR   27-MAR-2002;  2002US-0367550P.
PR   10-APR-2002;  2002US-0370227P.
PR   10-MAY-2002;  2002US-0378950P.
PR   24-MAY-2002;  2002US-0382617P.
PR   28-MAY-2002;  2002US-0383123P.
PR   05-JUN-2002;  2002US-0385708P.
PR   10-JUL-2002;  2002US-0394625P.
PR   24-JUL-2002;  2002US-0398018P.
PR   09-AUG-2002;  2002US-0402131P.
PR   13-AUG-2002;  2002US-0402708P.
PR   18-SEP-2002;  2002US-0411355P.
PR   18-SEP-2002;  2002US-0411426P.
PR   02-OCT-2002;  2002US-0414984P.
PR   11-OCT-2002;  2002US-0417611P.
PR   23-OCT-2002;  2002US-0420246P.
PR   05-NOV-2002;  2002US-0423623P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (DELI-) DELTA BIOTECHNOLOGY LTD.
PA   (PRIN-) PRINCIPIA PHARM CORP.
XX
PI   Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
DR   WPI; 2003-598517/56.
DR   P-PSDB; ADF17046.
XX
PT   New albumin fusion protein, useful for preparing a composition for
PT   treating diabetes mellitus.
XX
PS   Example 4; SEQ ID NO 2157; 24pp; English.
XX
CC   This invention relates to a novel albumin fusion protein having albumin
CC   or biological activity. Human serum albumin is responsible for a
CC   significant proportion of the osmotic pressure of serum and also
CC   functions as a carrier of endogenous and exogenous ligands. The fusion of
CC   albumin to a therapeutic protein may increase shelf-life and stability of
CC   the therapeutic protein. The albumin fusion protein of the invention may
CC   allow production of compositions with antidiabetic activity whilst the
CC   nucleotide sequence which encodes it may be useful for gene therapy. The
CC   albumin fusion protein is useful for preparing a composition for treating
CC   diabetes mellitus. The present sequence is a DNA sequence which encodes a
CC   therapeutic protein which was fused with human albumin to create a novel
CC   albumin fusion protein of the invention. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/publishedpct_sequences
XX
SQ   Sequence 489 BP; 170 A; 103 C; 98 G; 118 T; 0 U; 0 Other;

Query Match        74.0%; Score 299.6; DB 10; Length 489;
Best Local Similarity   84.1%;  Pred. No. 1.3e-83;
Matches  338;  Conservative   0;  Mismatches   64;  Indels   0;  Gaps   0;

Qy    4  CAAGGTCAAGAATCGCCACACATGATTAGAAATGGGTCAACTTATATAGATATTGTTGATCAGCTG 63
         ||||||||||| |||||| ||||||||||||| ||||| || | | |||||||||||||||||||
Db   88  CAAGGTCAAGGATCGCCAACATGATTAGAATGCCTCAACTTATAGATATTGTTGATCAGCTG 147

Qy   64  AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGAGATTTGAGACC 123
         ||||||||||||||||| |||||| |||||||||||| || ||| | ||||| | |||
Db  148  AAAAATTATGTGAATGAACTTGGTCCGCTTCCTGAATTTCTGCCAGCTCCAGAGATGTAGAGACA 207

Qy  124  AACTGTGAGTGGTCCGCTTTCTCCGTTTTCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
         |||||||||||||| ||||| ||| |||||||||||| |||| ||||| ||| || |||
Db  208  AACTGTGAGTGGTCAGCTTTTTTCGTGTTTTCAGAAAGGCCCAACTAAAGTCAGCAAATACA 267

Qy  184  GGTAACAACGAACGTATCATCAACGTTTCATTAAAAAACTGAACGTAAACCGCCGTCC 243
         || |||| |||  ||| ||||| ||| ||||| |||||| |||| |||  |||| ||||
Db  268  GGAAACAATGAAAAGTAAATCAAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC 327

Qy  244  ACCAACGCAGGTTCGTCGTCGTCAGAAAACCGTCTGACCTGCCGTCCGTCCTGTGATTCTTATGAG 303
         || ||| ||||   |    |   |||||| |||  |  |   || || ||| ||||||||||||||
Db  328  ACAAATGCAGGGAGGAAAGACAGAGAAACACAGACTAACATGCCCTTCATGTGTGATTCTTATGAG 387

Qy  304  AAAAAACCGCCGGAAAGAATTCCTGGAACGTTTCAAATCCCGCTGCAGAAAATGATTCAC 363
         ||||||||  ||  |||||||||| |   |||||||||| |  |  ||||||||||||| 
Db  388  AAAAAACCACCCAAAGAAATTCCTAGAAGATTCAAATCACTTCTCCAAAAAGATGATTCAT 447

Qy  364  CAGCACCTGTCCTCTCCGTACCCACGGTTCCGGAAGAGATTCCTGA 405
         ||||| ||||||||| || |||| |||| | |||||| ||||||||
Db  448  CAGCATCTGTCCTCTAGAACACACCGGAAGTGAAGAGATTCCTGA 489

RESULT 9

ID   ADV42801 standard; cDNA; 489 BP.
XX
AC   ADV42801;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 429.
XX
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
```

OS   Homo sapiens.
XX
PN   WO200410899-A2.
XX
PD   16-DEC-2004.
XX
PF   04-JUN-2004; 2004WO-US017686.
XX
PR   04-JUN-2003; 2003US-0475915P.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nicholson A, Vernon SD;
XX
DR   WPI; 2005-031682/03.
XX
PS   Claim 1; SEQ ID NO 429; 254pp; English.
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrininmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrininmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
XX
PT   New microarray comprising probes for genes involved in
PT   psychoneuroendocrininmune (PNI) activity, useful in diagnosing a
PT   condition associated with PNI activity, e.g., inflammatory or infectious
PT   diseases.
XX
SQ   Sequence 489 BP; 170 A; 103 C; 98 G; 118 T; 0 U; 0 Other;

Query Match   74.0%;   Score 299.6;   DB 14;   Length 489;
Best Local Similarity   84.1%;   Pred. No. 1.3e-83;
Matches 338;   Conservative   0;   Mismatches   64;   Indels   0;   Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||| |||||||| |||||||||||||||||||||||||
Db   88 CAAGGTCAAGATCGGCCACATGATTAGAAATGGGTCAACTTATAGATATTGTTGATCAGCTG 147

Qy   64 AAAAAATTATGTGAAATGACCTGGTTCCGGAATTCCTGCCAGCTCCGGAAGATGTTGAGACC 123
          |||||||||||||| ||||||||||||||||||||| |||||||||| ||||||||||
Db   148 AAAAAATTATGTGAATGACTTGGTCCCTGAAATTCTGCCAGCTCCAGAAGATGTTAGAGACA 207

Qy   124 AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCACTGAAAATCCCCAAACACC 183
          |||||||||||| |||||||| |||||||||||||| |||||||||||||||||||||
Db   208 AACTGTGAGTGGTCAGCTTTTTTCCGTTTTTCAGAAGGCCCAACTAAAGTCACCAAAATACA 267

Qy   184 GGTACAACGAACGTATCATCAACGTTTCCATTAAAAAAACGTAAAACCGCGGTCC 243
          |||||||||| |||||||| ||||||||| |||||| |||||||||| ||||
Db   268 GGAACAAATGAAAGGATAATCAAATGTATCAAATTAAAAAGCTGAAGAGGAAACCACCTTCC 327

Qy   244 ACCAACGCAGGTCGTCGTCGTTCAGAAAACACCGTCTGACCTCGTCTGTTTGATTCTTATGAG 303
          |||||||| |||||||| |||||||||| |||||| ||||||||||||| |||||||
Db   328 ACAAATGCAGGGAGGAAGACAGAAACACAGCCCTTCATGTGATTGATTCTTATGAG 387

Qy   304 AAAAAACCGCGAAAGAATTCCTGGAACGTTTCAAAATCCCCTGCCTGCGAGAAAATGATTCAC 363
          ||||| |||||||||||||||| |||| |||||| |||||||||| ||||||||||||
Db   388 AAAAAACCACCCAAAGAATTCCTAGAAAGATTCAAAATCACTTCTCCAAAAGATGATTCAT 447

Qy   364 CAGCACCTGTCCTCTCGTACCCACGCGTTCCGAAGAGATTCCTGA 405
          |||||||| |||| ||| |||||| |||| ||||||||||||||
Db   448 CAGCACTCGTCCTTCTAGAAACACACGCGAAGTGAAGAGATTCCTGA 489

OS   Homo sapiens.
XX
SQ   Sequence 489 BP; 170 A; 103 C; 98 G; 118 T; 0 U; 0 Other;

DT   22-JAN-2001 (first entry)
XX
DE   DNA encoding a human zalphall ligand polypeptide.
XX
KW   zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW   tumourigenesis; leukaemia; hematopoiesis; B cell tumour; 88.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   47..535
FT   /*tag= a
FT   /product= "zalphall"
XX
PN   WO200053761-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US006067.
XX
PR   09-MAR-1999;   99US-00264908.
PR   11-MAR-1999;   99US-00265992.
PR   01-JUL-1999;   99US-0142013P.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI   Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR   WPI; 2000-565600/52.
DR   P-PSDB; AAB18623.
XX
PT   New human cytokine, designated zalphall ligand, useful for stimulating
PT   the proliferation and/or development of hematopoietic cells in vitro and
PT   in vivo, and for treating tumorigenesis.
XX
CC   The present sequence encodes a human zalphall ligand polypeptide, which
CC   is a cytokine. The zalphall ligand is useful for stimulating the
CC   proliferation and development of haematopoietic cells in vitro and in
CC   vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC   for cloning the zalphall gene. The zalphall ligand is useful for treating
CC   tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for
CC   treating leukaemias and lymphomas. Antagonists against zalphall ligand
CC   are useful as research reagents for characterizing ligand-receptor
CC   interaction. Antagonists are also useful for inhibiting expansion,
CC   proliferation, activation and differentiation of cells involved in
CC   regulating hematopoiesis. The zalphall ligand may also be used to
CC   stimulate an immune response against B cell tumour, a virus, a parasite
CC   or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC   agonists and antibodies are also useful for the detection, diagnosis,
CC   prevention, and treatment of diseases associated with a zalphall ligand
CC   genetic defect
XX
PS   Claim 14; Page 204-205; 256pp; English.
XX
SQ   Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match   74.0%;   Score 299.6;   DB 3;   Length 642;
Best Local Similarity   84.1%;   Pred. No. 1.5e-83;
Matches 338;   Conservative   0;   Mismatches   64;   Indels   0;   Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||| |||||||| |||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGGCCACATGATTAGAAATGGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAAATTATGTGAAATGACCTGGTTCCGGAATTCCTGCCAGCTCCGGAAGATGTTGAGACC 123
          |||||||||||||| ||||||||||||||||||| |||||||||| ||||||||||
Db   194 AAAAAATTATGTGAATGACTTGGTCCCTGAAATTCTGCCAGCTCCAGAAGATGTTAGAGACA 253

Qy   124 AACTGTGAGTGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCACTGAAAATCCGCCAAACACC 183
          |||||||||||| |||||||| |||||||||||||| |||||||||||||| |||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTTCAGAAGGCCCAACTAAAGTCAGCAAAATACA 313

Qy 184 GGTAACACGAACGAACTATCATCAACGGTTTCATTAAAAAACTGAAAACGTAAACCCGCGTCC 243
Db 314 GGAAACAATGAAAAGGATAATCAATCGTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC 373
XX
Qy 244 ACCAACGCAGGTCGTCGTCGTCAGAAACACACCGTGCCTGCCGTCGTTGTGATTCTTATGAG 303
Db 374 ACAAATGCAGGGAGGAAGAGACAGAAACACACAGA 433
XX
Qy 304 AAAAAACGCGGAAAGAATTCCTGGAACGGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
Db 434 AAAAAACCACCCAAAGAAATTCCTAGAAGAATTCAAATCACTTCTCCAAAAGATGATTCAT 493
XX
Qy 364 CAGCACCTGTCCTCTCGTTACCCACGGTTCCGAAGAGTGAAAGAGATTCCTGA 405
Db 494 CAGCATCTGTCCTCTAGAACACACCGGAAGTGAAAGAGATTCCTGA 535

RESULT 11
AAS20637

ID   AAS20637 standard; cDNA; 642 BP.
XX
AC   AAS20637;
XX
DT   09-APR-2002 (first entry)
XX
DE   cDNA encoding human zalpha11 Ligand polypeptide.
XX
KW   Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW   natural killer cell proliferation; T-cell proliferation;
KW   B-cell proliferation; anti-tumour response; immune system;
KW   immunostimulant; cytostatic; human; gene therapy; hPBCS;
KW   activated human peripheral blood cell; ss.
XX
OS   Homo sapiens.
XX
FH
FT   Key   Location/Qualifiers
FT   CDS   47..535
FT   /tag= a
FT   /product= "zalpha11 Ligand"
FT   sig_peptide   47..139
FT   /tag= b
FT   mat_peptide   140..532
FT   /tag= c
XX
PN   US6307024-B1.
XX
PD   23-OCT-2001.
XX
PF   09-MAR-2000; 2000US-00522217.
XX
PR   09-MAR-1999; 99US-0123547P.
PR   11-MAR-1999; 99US-0123904P.
PR   01-JUL-1999; 99US-0142013P.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI   Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR   WPI; 2002-040208/05.
DR   P-PSDB; AAU11965.
XX
PT   New zalpha11 ligand polypeptides and polynucleotides, useful for
PT   stimulating proliferation, differentation, activation, and/or induction
PT   of inhibition of specialized cell function, or for stimulating an
PT   antigenic response.
XX
PS   Example 7; Col 123-126; 105pp; English.
XX
CC   The present invention relates to the isolation of a novel cytokine,
CC   zalpha11 Ligand and the polynucleotide encoding it. The invention also
CC   gives the sequence for the zalpha11 receptor and the polynucleotide
CC   encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of

CC   natural killer (NK) cells or NK cell progenitors, the activation of NK
CC   cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC   anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC   reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC   zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC   bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC   be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC   and in gene therapy. Zalpha11 Ligand may also be used to identify
CC   inhibitors of its activity, to enhance the generation of anti-tumour
CC   responses with or without the infusion of donor lymphocytes, and to
CC   activate or stimulate the immune system. The present sequence encoding
CC   for human zalpha11 Ligand polypeptide is isolated from a cDNA library
CC   from activated human peripheral blood cells (hPBCS)
XX
SQ   Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match   74.0%; Score 299.6; DB 6; Length 642;
Best Local Similarity   84.1%; Pred. No. 1.5e-83;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACCATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGCCACCATGATTAGAAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy   64 AAAAAATTATGTGAATGACCTGGTTCCGGAAATTCCTGCCGCGGTCCTCCGGAAGAGTTGAGACC 123
          ||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   194 AAAAATTATGTGAATGACCTGGTTCCGGAAATTCCTGCCGCGGTCCTCCGGAAGAGTTGAGACA 253

Qy   124 AACTGTGAGTGGTCCCGCTTTCTCCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGGCAAAACACC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   254 AACTGTGAGTGGTCAGCTTTTTTCCCTGTTTTTCAGACGAGGGCCCAACTAAGTCAGCCAAATACA 313

Qy   184 GGTAACACGAACGAACTATCATCAACGTTTCATTAAAAAAACTGAAAACGTAAACCGCGTCC 243
          ||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||
Db   314 GGAAACAATGAAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC 373

Qy   244 ACCAACGCAGGTCGTCGTCGTCAGAAACACACCGTGCCTGCCGTCGTTGTGATTCTTATGAG 303
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   374 ACAAATGCAGGGAGGAAGAGACAGAAACACACAGACTAACATGCCCTTCATGTGATTCTTATGAG 433

Qy   304 AAAAAACGCGGAAAGAATTCCTGGAACGGTTTCAAATCCCTGCTGCAGAAAATGATTCAC 363
          ||||||| ||||||||||||||||| |||| ||||||||| ||||||||||||||||||
Db   434 AAAAAACCACCCAAAGAAATTCCTAGAAGAATTCAAATCACTTCTCCAAAAGATGATTCAT 493

Qy   364 CAGCACCTGTCCTCTCGTTACCCACGGTTCCGAAGAGTGAAAGAGATTCCTGA 405
          ||||| |||||||||| ||||||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACCGGAAGTGAAAGAGATTCCTGA 535

RESULT 12
AAD47852

ID   AAD47852 standard; DNA; 642 BP.
XX
AC   AAD47852;
XX
DT   27-AUG-2003 (first entry)
XX
DE   Human interleukin-21 (IL-21) DNA.
XX
KW   Interleukin-21; IL-21; antagonist; cancer; inflammatory;
KW   autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW   systemic lupus erythematosus; myasthenia gravis; diabetes; human;
KW   zalpha11 ligand; ds.
XX
OS   Homo sapiens.
XX
FH
FT   Key   Location/Qualifiers
FT   CDS   47..535
FT   /tag= a
FT   /product= "IL-21"
XX
PN   WO200040313-A2.

Left column:

```
PD   15-MAY-2003.
XX
PF   28-OCT-2002; 2002WO-US0034502.
XX
PR   05-NOV-2001; 2001US-0337586P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR, West JW, Novak JE;
XX
DR   WPI; 2003-441547/41.
DR   P-PSDB; AAE14932.
XX
PT   New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
PT   and treating disorders with aberrant expression or activity of the IL-21
PT   polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
PT   diabetes.
XX
PS   Disclosure; Page 52-53; 71pp; English.
XX
CC   The invention relates to polynucleotides and polypeptides of interleukin-
CC   21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
CC   that is not detectable in receptor binding studies. The antagonists of
CC   the invention have mutations in the D helix of the IL-21 molecule, and
CC   can be used to inhibit the activity of IL-21 with its cognate receptor.
CC   The IL-21 antagonists are useful for diagnosing and treating disorders
CC   involving the aberrant expression or activity of the IL-21 polypeptide,
CC   such as cancer, inflammatory and autoimmune disorders, including
CC   rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
CC   myasthenia gravis and diabetes. The polypeptides can also be used to
CC   prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
CC   and for enhancing in vivo killing of target tissues. The present sequence
CC   is human IL-21 (originally designated zalpha11 ligand) DNA
SQ   Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match           74.0%;  Score 299.6;  DB 9;  Length 642;
Best Local Similarity 84.1%;  Pred. No. 1.5e-83;
Matches 338; Conservative  0; Mismatches  64; Indels  0; Gaps  0;

Qy        4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATAGATAATTGTTGATCAGCTG   63
            |||||||||||||||||||||||||||||  |||||||| ||||||||||||||||||||||
Db      134 CAAGGTCAAGAATCGCCACATGATTAGAAATGCGTCAACTTATAGATAATTGTTGATCAGCTG  193

Qy       64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTCCGCGGCTCCCGGAAGATGTTTGAGACC  123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      194 AAAAATTATGTGAATGACCTTGGTCCCTGAATTCTCCCAGCTCCCAGAGATGTAGAGACA   253

Qy      124 AACTGTGAGTGGTCCGCTTTCTCCCTGTTTCCAGAAAAGCCACTGAAATCCGCAAACACC  183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      254 AACTGTGAGTGGTCAGCTTTTTCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA   313

Qy      184 GGTACAACGAACGTATCATCAACAGCGTTCCATTAAAAACGTAAAACGTAAACCGCGTCC   243
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      314 GGAAACAAATGAAAGGATAATCAAATGTTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC  373

Qy      244 ACCAACGCACAGGTCGTCGTCAGAAAACACCGTCTGACCTGCGCGTCCGTTGATTCTTATGAG   303
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      374 ACAAATGCAGGGAGAAGACACGAAAAACACAGCCCTTCACATGGCCCTGCAGAAAATGATTCAC  433

Qy      304 AAAAAACCGCCGAAAGAGAATTCCTGGAACGGTTTCAAATCCCTGCTGCAGAAAATGATTCAC  363
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      434 AAAAAACCACCCAAAGAATTCCTAGAAGAATTCAAATCACTTCTCCAAAAGATGATTCAT   493

Qy      364 CAGCACCTTGTCCTCTCCGTACCCACGCGTTCCCAAAGATTCCTGA   405
            |||||||||||||||||||||||||||||||||||||||||||||
Db      494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA   535
```

Right column:

```
AC   ADH44571;
XX
DT   25-MAR-2004 (first entry)
XX
DE   Human cDNA encoding zalpha11 ligand.
XX
KW   Human; ss; Zalpha11 ligand; Zalpha11 receptor; immune response;
KW   tumour progression; metastasis; tumour stasis; haematopoietic tumour;
KW   lymphoma; B cell tumour; systemic lupus erythematosus;
KW   rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
KW   immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
XX
OS   Homo sapiens.
XX
PN   US6605272-B2.
XX
PD   12-AUG-2003.
XX
PF   03-AUG-2001; 2001US-00923246.
XX
PR   09-MAR-1999;  99US-01235547P.
PR   11-MAR-1999;  99US-01239904P.
PR   01-JUL-1999;  99US-01420103P.
PR   09-MAR-2000; 2000US-00522217.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI   Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR   WPI; 2003-895283/82.
XX
PT   Example 7; SEQ ID NO 1; 103pp; English.
XX
PS   The invention relates to stimulating an immune response in a mammal
CC   exposed to an antigen or pathogen comprises administering a composition
CC   comprising mature zalpha11 ligand polypeptide comprising residues 32-162
CC   of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an
CC   immune response in a mammal exposed to an antigen or pathogen
CC   (comprising: (a) determining (in)directly the level of antigen or
CC   pathogen present in the mammal; (b) administering a composition
CC   comprising zalpha11 ligand polypeptide in a pharmaceutical vehicle; (c)
CC   determining (in)directly the level of antigen or pathogen in the mammal;
CC   and (d) comparing the antigen or pathogen level in (a) with (b), where a
CC   change in the level indicates stimulation of immune response), and
CC   stimulating an immune response in a mammal exposed to an antigen or
CC   pathogen (comprising: (a) determining a level of antigen- or pathogen-
CC   specific antibody; (b) administering a composition comprising zalpha11
CC   ligand polypeptide in a pharmaceutical vehicle; (c) determining post
CC   administration level of the antigen- or pathogen-specific antibody; and
CC   (d) comparing the level of the antibody in (a) with (b), where an
CC   increase in the antibody level indicates stimulation of immune response).
CC   The method is useful for stimulating an immune response in a mammal
CC   exposed to an antigen or pathogen, and for enhancing anti-tumour activity
CC   resulting in a reduction in tumour progression, decrease in metastasis,
CC   or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
CC   or a B cell tumour. The zalpha11 ligand is useful for treating a wide
CC   range of diseases arising from defects in the immune system, e.g.
CC   systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
CC   diabetes, for boosting immunity to infectious diseases, treating
CC   immunocompromised patients, such as HIV+ patients and in improving
CC   vaccines. The present sequence is a human zalpha11 ligand cDNA (or
CC   fragment).
XX
SQ   Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match           74.0%;  Score 299.6;  DB 10;  Length 642;
Best Local Similarity 84.1%;  Pred. No. 1.5e-83;
```

Bottom left block:

```
RESULT 13
ID   ADH44571
XX
ID   ADH44571 standard; cDNA; 642 BP.
XX
```

Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy     4 CAAGGTCAAGATCGGCCACATGATTAGAATGCGGTCAACTTATAGATATTGTTGATCAGCTG   63
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGGCCACATGATTAGAATGCGGTCAACTTATAGATATTGTTGATCAGCTG  193

Qy    64 AAAAAATTATGTGAATGAAAGACCTGGGTTCCGGAAGTTCCTGCGCGGATGTTGAGACC  123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAAATTATGTGAATGAAAGACCTGGGTTCCGGAAGTTCCTGCGCGGATGTTGAGACA  253

Qy   124 AACTGTGACTGGGTCAGCTGTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAACACC  183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGACTGGGTCAGCGTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA  313

Qy   184 GGTTAACAACGAACGTATCATCAACGTTTCCATTAAAAACTGAAACGTAAACCGCGCCGTCC  243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAACAATGAAACGGATAATCAATGTATCAATTAAAAAGTCTGAAGAGGAAAACCACCTTCC  373

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAAACACCTGTGACCTGGGGCCGCCCTCGTGTTCTTATGAG  303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ACAAATGCAGGAGGAAGACAGAAAACAGACTAACAACCGTGAAAGAGGAAAACCACTTCC  433

Qy   304 AAAAAACCCCGCGAAAAGAATTCCTGGAAACGTTTCAAAATCCCTGCCGAGAAAATGATTCAC  363
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAACCCAAAGAAATTCCTAGAAAAGAATTCACTTCTCCAAAAGATGATTCAT  493

Qy   364 CAGCACCTGTCCTCTCGTACCCACCGGTTCCGAAGAGATTCCTGA  405
         |||||||||||||||||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA  535
```

RESULT 14
ID   ADI00907   standard; cDNA; 642 BP.
XX
AC   ADI00907;
XX
DT   22-APR-2004 (first entry)
XX
DE   Immunity-related human zalpha11 ligand cDNA.
XX
KW   zalpha11 ligand; immunity; infectious disease; immunocompromised patient;
KW   HIV; vaccine; human; ss; gene.
XX
OS   Homo sapiens.
XX
XX
PN   US2003125524-A1.
XX
PD   03-JUL-2003.
XX
PF   15-NOV-2002; 2002US-00295723.
XX
PR   09-MAR-2000; 2000US-00522217.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI   Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR   WPI; 2003-811003/76.
DR   P-PSDB; ADI00908.
XX
PT   New zalpha11 ligand polypeptides, useful for boosting immunity to
PT   infectious diseases, and treating immunocompromised patients, such as
PT   human immunodeficiency virus (HIV) patients, or in improving vaccines.
XX
PS   Claim 19; SEQ ID NO 1; 113pp; English.
XX
CC   The invention relates to a novel isolated zalpha11 ligand polypeptide.
CC   The polypeptide of the invention may be useful for boosting immunity to
CC   infectious diseases and treating immunocompromised patients, such as HIV
CC   patients, as well as in improving vaccines. The current sequence is that
CC   of the human zalpha11 ligand cDNA of the invention.

XX
SQ   Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match   74.0%; Score 299.6; DB 10; Length 642;
Best Local Similarity   84.1%; Pred. No. 1.5e-83;
Matches 338; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

```
Qy     4 CAAGGTCAAGATCGGCCACATGATTAGAATGCGGTCAACTTATAGATATTGTTGATCAGCTG   63
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 CAAGGTCAAGATCGGCCACATGATTAGAATGCGGTCAACTTATAGATATTGTTGATCAGCTG  193

Qy    64 AAAAAATTATGTGAATGAAAGACCTGGGTTCCGGAAGTTCCTGCGCGGATGTTGAGACC   123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   194 AAAAAATTATGTGAATGAAAGACCTGGGTTCCGGAAGTTCCTGCGCGGATGTTGAGACA  253

Qy   124 AACTGTGACTGGGTCGTGTTCCCCTTTCTCCGTGTTTCCAGAAAGCCCAGCTGAAAATCCGGCAAACC  183
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   254 AACTGTGACTGGGTCGTGTTCCCCTTTCTCCGTGTTTCCAGAAAGCCCAGCTGAAAATCCGGCAAACC  313

Qy   184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAAACGTAAACCGCGCCTCC  243
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   314 GGAAACAATGAAACGGATAATCAATGTATCAATTAAAAAGTCTGAAGAGGAAAACCACCTTCC  373

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAAACACCTGTGACCTGGGGCCGCCCTCGTGTTCTTATGAG  303
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   374 ACAAATGCAGGAGGAAGACAGAAAACAGACTAACAACCGTGAAAGAGGAAAACCACTTCC  433

Qy   304 AAAAAACCCCGCGAAAAGAATTCCTGGAAACGTTTCAAAATCCCTGCCGAGAAAATGATTCAC  363
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   434 AAAAAACCCAAAGAAATTCCTAGAAAAGAATTCACTTCTCCAAAAGATGATTCAT  493

Qy   364 CAGCACCTGTCCTCTCGTACCCACCGGTTCCGAAGAGATTCCTGA  405
         |||||||||||||||||||||||||||||||||||||||||||||
Db   494 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA  535
```

RESULT 15
ID   ADH10500   standard; DNA; 642 BP.
XX
AC   ADH10500;
XX
DT   11-MAR-2004 (first entry)
XX
DE   Human interleukin-21 (IL-21) encoding DNA.
XX
KW   IL-21; interleukin-21; cytostatic; virucide; antiinflammatory;
KW   hepatotropic; neuroprotective; muscular; respiratory; antiarthritic;
KW   antibacterial; anti-HIV; gene therapy; cancer; human; gene; ds.
XX
OS   Homo sapiens.
XX
XX
FH   Key   Location/Qualifiers
FT   CDS   47..535
FT   /*tag= a
FT   /product= "interleukin-21"
XX
PN   WO2003103589-A2.
XX
PD   18-DEC-2003.
XX
PF   06-JUN-2003; 2003WO-US017808.
XX
PR   07-JUN-2002; 2002US-0387127P.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Nelson AJ, Hughes SD, Holly RD, Kindsvogel WR;
XX
DR   WPI; 2004-062206/06.
DR   P-PSDB; ADH10501.
XX
PT   Treating Non-Hodgkin's lymphoma, cancer or infection comprises

```
PT  administering to the subject a polypeptide having a functional activity
PT  of interleukin-21.
XX
PS
XX
SQ  Disclosure; SEQ ID NO 1; 154pp; English.

CC  The invention relates to treating Non-Hodgkin's lymphoma, cancer or
CC  infection and involves administering to the subject a polypeptide having
CC  a functional activity of interleukin-21 (IL-21). The methods are useful
CC  for treating Non-Hodgkin's lymphoma; cancer such as renal cell carcinoma,
CC  epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and
CC  colon cancer; viral infection such as AIDS, Hepatitis B or C virus,
CC  gastroenteritis, haemorrhagic diseases, enteritis, carditis,
CC  encephalitis, paralysis, bronchiolitis, upper or lower respiratory
CC  disease, respiratory papillomatosis, arthritis, disseminated disease,
CC  meningitis, and mononucleosis; or bacterial infection, such as an
CC  infection by a bacteria selected from chlamydiae, listeriae, helicobacter
CC  pylori, mycobacterium, mycoplasma, salmonella, and shigella, or sudden
CC  acute respiratory syndrome caused by a coronavirus, Herpes Simplex
CC  viruses, Epstein-Barr virus, Cytomegalovirus, Pox viruses, Papilloma
CC  virus, Adenovirus, Poliovirus, Orthomyxoviruses, Paramyxoviruses,
CC  Influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses.
CC  The present sequence represents a DNA encoding a human IL-21 polypeptide.
XX
XX
SQ  Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match             74.0%;  Score 299.6;  DB 12;  Length 642;
Best Local Similarity   84.1%;  Pred. No. 1.5e-83;
Matches  338; Conservative   0; Mismatches  64;  Indels   0;  Gaps   0;

Qy       4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 193

Qy      64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAGAGTGTTGAGACC 123
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCCAGCTCCAGAGATGTAGAGACA 253

Qy     124 AACTGTGTGAGTGGTGTCCCGCTTTCTCCGTGTTTCCAGAAAGCCCAGCTGAAATCCCGCAAAACACC 183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 AACTGTGAGTGGTGTCAGCTTTTTTCCCTGTTTTTCAGAAGGGCCCAACTAAAGTCAGCAAAATACA 313

Qy     184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 GGAAACAAATGAAAAGGATAATCAAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC 373

Qy     244 ACCAACGCAGGTCGTCGTTCAGAAAACACCGTCTGACCTGCCCCGGTCCTGTGATTCTTATGAG 303
           || |||||||||||||||| | |||||||||||||||||||||||||||||||||||||||
Db     374 ACAAATGCAGGGAAGACAGAGAACACAGACTAACATGCCCTTCATCGTGATTCTTTATGAG 433

Qy     304 AAAAAACCGCCGAAAAGAAATTCTGGAACGTTTCAAAATCCCTCCTGCTGCAGAAAATGATTCAC 363
           |||||| |||||||||||||||||||||||||||||||||| | |||||||||||||||||
Db     434 AAAAAACCACCCAAAAGAATTCCTAGAAAGATTCAAAATCACTTCTCCAAAAGATGATTCAT 493

Qy     364 CAGCACCTGTTCCTTCGTACCCACGGGTTCCGAAGGATTCCTGA 405
           ||||| |||||||| |||||||||||||||||||||||||||||
Db     494 CAGCATCTGTTCCTTCTAGAACACACGGAAGTGAAGAATTCCTGA 535
```

Search completed: August 7, 2006, 13:13:21
Job time : 523 secs

```
OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.9
                    Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:             August 7, 2006, 12:06:06 ; Search time 4431 Seconds
                                               (without alignments)
                                               5111.110 Million cell updates/sec

Title:              US-10-735-149-27
Perfect score:      405
Sequence:           1 atgcaaggtcaagatcgcca.........acggttccgaagattcctga 405

Scoring table:      IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched:           48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters:          96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
                1:  gb_est1:*
                2:  gb_est3:*
                3:  gb_est4:*
                4:  gb_est5:*
                5:  gb_est6:*
                6:  gb_htc:*
                7:  gb_est2:*
                8:  gb_est7:*
                9:  gb_est8:*
               10:  gb_est9:*
               11:  gb_gss1:*
               12:  gb_gss2:*
               13:  gb_gss3:*
               14:  gb_gss4:*

                Pred. No. is the number of results predicted by chance to have a
                score greater than or equal to the score of the result being printed,
                and is derived by analysis of the total score distribution.

                                SUMMARIES
                                                                %
Result                          Query
No.    Score   Match Length  DB  ID        Description
----   -----   ------------  --  --        -----------
   1   299.6   74.0    489   14  AY417615   AY417615 Homo sapi
 c 2   299.6   74.0    566    5  CD559455   CD559455 AGENCOURT
 c 3   299.6   74.0    573    5  CD559609   CD559609 AGENCOURT
 c 4   299.6   74.0    581    5  CD559459   CD559459 AGENCOURT
 c 5   299.6   74.0    582    5  CD559457   CD559457 AGENCOURT
 c 6   299.6   74.0    582    5  CD559461   CD559461 AGENCOURT
 c 7   299.6   74.0    583    5  CD559456   CD559456 AGENCOURT
 c 8   299.6   74.0    583    5  CD559612   CD559612 AGENCOURT
 c 9   299.6   74.0    592    5  CD559614   CD559614 AGENCOURT
 c 10  299.6   74.0    599    5  CD559610   CD559610 AGENCOURT
   11  298     73.6    600    5  CD559613   CD559613 AGENCOURT
 c 12  296.4   73.2    581    5  CD559460   CD559460 AGENCOURT
 c 13  294.2   72.6    489   14  AY417616   AY417616 Pan trogl
 c 14  292.2   72.2    551    8  CR988723   CR988723 AGENCOURT
 c 15  283.2   69.9    608    5  CD559611   CD559611 AGENCOURT
 c 16  252.8   62.4    749    5  CD559458   CD559458 AGENCOURT
   17  195.8   48.3    567    5  BP369699   BP369699 AGENCOURT
   18  167.6   41.4    438   14  AY417617   AY417617 Mus muscu
   19  113.2   28.0    421    5  CJ141332   CJ141332 CJ141332
```

```
                                ALIGNMENTS

RESULT 1
AY417615
LOCUS       AY417615                 489 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Homo sapiens IL21 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY417615
VERSION     AY417615.1  GI:39773575
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 489)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..489
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>489
                     /gene="IL21"
                     /locus_tag="HCM6283"
ORIGIN
```

```
 c 20  100.8   24.9   450    4   BY580318   BY580318 BY580318
 c 21   84.2   20.8   756   13   DU302657   DU302657 109844828
 c 22   78.8   19.5   681   13   C2424877   C2424877 1020580 R
 c 23   78.8   19.5   709   13   C2419965   C2419965 1015668 R
 c 24   78.8   19.5   735   13   C2427169   C2427169 1022872 R
 c 25   67.2   16.6   539   12   B2937073   B2937073 CH240.61E
 c 26   59.6   14.7   339    4   BY214337   BY214337 BY214337
 c 27   59.6   14.7   363    9   BY212756   BY212756 BY212756
 c 28   59.6   14.7   426    4   BY211567   BY211567 BY211567
 c 29   59.6   14.7   535    1   AZ248993   AZ248993 RPCI-23-4
 c 30   59.6   14.7   535   11   AA764063   AA764063 vw09e02.r
 c 31   59.6   14.7   697    3   BY750468   BY750468 Mus muscu
 c 32   57.6   14.2   2338   6   AK155984   AK155984 Mus muscu
 c 33   57.6   14.2   365    4   BY220565   BY220565 BY220565
 c 34   57.4   14.2   812    2   BI561560   BI561560 603256262
 c 35   50      12.3   584   13   C2026087   C2026087 CH240_498
 c 36   46.4   11.5   880   14   CT053999   CT053999 Sus scrof
 c 37   40.4   10.0   629   11   AZ435999   AZ435999 1M0223N20
 c 38   38.8    9.6   1302   2   BY213229   BY213229 BY213229
 c 39   37.8    9.3   647   11   BZ572734   BZ572734 msh2_2773
 c 40   37.8    9.3   1066  10   BH013521   BH013521 TDGAY96TH
 c 41   37.2    9.2   503   10   DV013822   DV013822 DV013822
 c 42   37.2    9.2   884   14   BH124149   BH124149 RPCI-24-3
 c 43   36      8.9   1441   9   DN506U0    CNS006U0 Drosophil
 c 44   36      8.9   884   14   DN737022   DN737022 CNB90-E02
 c 45   35.8    8.8   856   12   CC509666   CC509666 CH240_352
```

RESULT 2

CD559455/c

```
Query Match         74.0%;  Score 299.6;  DB 14;  Length 489;
Best Local Similarity   84.1%;  Pred. No. 9.5e-83;
Matches 338;  Conservative  0;  Mismatches  64;  Indels  0;  Gaps  0;

Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGGGTCAACTTATAGATATTGTTGATCAGCTG 63
        |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   88 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 147

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGTCCGGAAGAGTTGAGACC 123
        ||||||||||||||||||| |||| ||| |||| |||||| | ||| |||||||||| |
Db  148 AAAAATTATGTGAATGACTTGGTCCCTGNAATTNCTGCCAGCTCCAGAGAGTTGAGACA 207

Qy  124 AACTGTGAGTGGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAACC 183
        |||||||||||||||  || ||| | ||||| ||| || | | |||  || |||||||||
Db  208 AACTGTGAGTGGGTCAGCTTTTTCCGTGTTTCAGAGAGGCGCCAAACTAAAGTCAGCAAATACA 267

Qy  184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCCGCGTCC 243
        || ||||| |||  | || |||||||| | | |||||||||||| | |  ||| || |||
Db  268 GGAAACAATGAAAGAATAATCAAACGTTATCAAATAAAAAACTGAGAGGGAAAACCACCTTCC 327

Qy  244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCGACCTGCCGTCCTGTGATTCTTATGAG 303
        || |||| |||| |  |  |||||||| |  ||| |||||   | ||||||||||||||
Db  328 ACAAATGCAGGGAGGGAGAAGCAGAAAAACAGAGTAACATGCCCTTTCATGTGATTCTTATGAG 387

Qy  304 AAAAAACCGCCGAAAGAAGAATTCCTGCCGTCGTCTGCAGAAAAATGATTCAC 363
        |||||| || | ||||||||||||| | |    |  ||| ||| |||||||| |
Db  388 AAAAAAACCACCAAAAGAATTCCTAGAAAAGATTCAAAATCACTTCTCCAAAAGATGATTCAT 447

Qy  364 CAGCACCTGTCCTCTCGTACCCACCGGTTCCGAAGATTCCTGA 405
        ||||| |||||||||   | ||| |||  | | ||||||||||
Db  448 CAGCATCTGTCCTCTPAGAAACACACGGAAGTGAAGAATTCCTGA 489
```

ORIGIN
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

```
LOCUS       CD559455               566 bp    mRNA    linear   EST 11-JUN-2003
DEFINITION  AGENCOURT 14497025 NIH_MGC 195 Homo sapiens cDNA clone
            IMAGE:6971867 3', mRNA sequence.
ACCESSION   CD559455
VERSION     CD559455.1  GI:31585523
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 566)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2  row: g  column: 10
            High quality sequence stop: 566.
FEATURES             Location/Qualifiers
     source          1..566
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971867"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
```

RESULT 3

CD559609

```
Query Match         74.0%;  Score 299.6;  DB 5;  Length 566;
Best Local Similarity   84.1%;  Pred. No. 9.8e-83;
Matches 338;  Conservative  0;  Mismatches  64;  Indels  0;  Gaps  0;

Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGGGTCAACTTATAGATATTGTTGATCAGCTG 63
        |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  433 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 374

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGTCCGGAAGAGTTGAGACC 123
        ||||||||||||||||||| |||| ||| |||| |||||| | ||| |||||||||| |
Db  373 AAAAATTATGTGAATGACTTGGTCCCTGNAATTNCTGCCAGCTCCAGAGAGTTGAGACA 314

Qy  124 AACTGTGAGTGGGTCCGCTTTCTCCTGTTTCCAGAAAGCCCAGCTGAAAATCCGCAAACC 183
        |||||||||||||||  || ||| | ||||| ||| || | | |||  || |||||||||
Db  313 AACTGTGAGTGGGTCAGCTTTTTCCGTGTTTCAGAGAGGCGCCAAACTAAAGTCAGCAAATACA 254

Qy  184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAACGTAAACCCGCGTCC 243
        || ||||| |||  | || |||||||| | | |||||||||||| | |  ||| || |||
Db  253 GGAAACAATGAAAGAATAATCAAACGTTATCAAATAAAAAACTGAGAGGGAAAACCACCTTCC 194

Qy  244 ACCAACGCAGGTCGTCGTCAGAAACACCGTCGACCTGCCGTCCTGTGATTCTTATGAG 303
        || |||| |||| |  |  |||||||| |  ||| |||||   | ||||||||||||||
Db  193 ACAAATGCAGGGAGGGAGAAGCAGAAAAACAGAGTAACATGCCCTTTCATGTGATTCTTATGAG 134

Qy  304 AAAAAACCGCCGAAAGAAGAATTCCTGCCGTCGTCTGCAGAAAAATGATTCAC 363
        |||||| || | ||||||||||||| | |    |  ||| ||| |||||||| |
Db  133 AAAAAAACCACCAAAAGAATTCCTAGAAAAGATTCAAAATCACTTCTCCAAAAGATGATTCAT 74

Qy  364 CAGCACCTGTCCTCTCGTACCCACCGGTTCCGAAGATTCCTGA 405
        ||||| |||||||||   | ||| |||  | | ||||||||||
Db   73 CAGCATCTGTCCTCTPAGAAACACACGGAAGTGAAGAATTCCTGA 32
```

```
LOCUS       CD559609               573 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT 14496932 NIH_MGC 195 Homo sapiens cDNA clone
            IMAGE:6971866 5', mRNA sequence.
ACCESSION   CD559609
VERSION     CD559609.2  GI:38558943
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 573)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585677.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
```

RESULT 4

Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 09
High quality sequence stop: 573.

FEATURES   Location/Qualifiers
     source   1..573
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971866"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."

ORIGIN

Query Match   74.0%;   Score 299.6; DB 5;   Length 573;
Best Local Similarity   84.1%;   Pred. No. 9.9e-83;
Matches 338;   Conservative   0;   Mismatches 64;   Indels   0;   Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 198

Qy   64 AAAAATTATGTGAATGAACTGGTCCCTGTTTCCGGAAATTCCTGCCGGAAGATGTTGAGACC 123
           |||||||||||||||||||| ||||| |||||| ||| || |||||||||||| |||||
Db   199 AAAAATTATGTGAATGACTGGTCCCTGAATTTCTGCCCAGAGATGTAGAGACA 258

Qy   124 AACTGTGAGTGGTCCGCCTTTCTCCTGTTTCCAGAAGAGCCAGCTGAAATCCGCAAACACC 183
           |||||||||||| |||| |||||| ||||| |||||| ||||||||||||| ||||||||
Db   259 AACTGTGAGTGTCAGCTTTTTCCTGTTTTCAGAAGGCCCAACTAAAGTCAGCAAATACA 318

Qy   184 GGTAACAACGAAACGTATCACACAGTTTCCATTAAAAAACTGAAACGTAAACCGCGCGTCC 243
           ||| || |||||| |||| |||| |||||||| |||||||||||| |||||||||||||
Db   319 GGAAACAATGAAAGGAATAATTCAAATTAAAAACTGAAGAGAAAACCACCTTCC 378

Qy   244 ACCAACGCAGGTCGTCGTCGTCGTCTGACCTCGCCGTCCGTTCGTTGATTCTTATGAG 303
           ||||| ||| ||||| ||| ||| ||||||| ||||||||||| |||||||| ||||||
Db   379 ACAAATGCAGGGAGGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAG 438

Qy   304 AAAAAACCGCGGAAAGAAATTCCTGGAACAGTTTCAAAATCCCTGCTGCCAGAAAATGATTCAC 363
           ||||| |||| |||||||||| |||| || ||||||| ||| || ||||| |||||||| ||
Db   439 AAAAACACCCAAGAATTCCTAGAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT 498

Qy   364 CAGCACCTGTTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
           ||| ||||||||| ||||| |||| |||| |||| |||||||||
Db   499 CAGCATTCGTCCTCTTGAAACACACGGAAGTGAAGATTCCTGA 540

Qy   364 CAGCACCTGTTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405

Db   499 CAGCATTCGTCCTCTTGAAACACACGGAAGTGAAGATTCCTGA 540

CD559459/c
LOCUS   CD559459   581 bp   mRNA   linear   EST 19-NOV-2003
DEFINITION AGENCOURT 14967771 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971863 5', mRNA sequence.
ACCESSION   CD559459
VERSION   CD559459.2 GI:38453485
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 581)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585527.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2 row: g column: 06
            High quality sequence start: 21.
            High quality sequence stop: 581.
FEATURES   Location/Qualifiers
     source   1..581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."

ORIGIN

Query Match   74.0%;   Score 299.6; DB 5;   Length 581;
Best Local Similarity   84.1%;   Pred. No. 9.9e-83;
Matches 338;   Conservative   0;   Mismatches 64;   Indels   0;   Gaps   0;

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 389

Qy   64 AAAAATTATGTGAATGAACTGGTCCCTGTTTCCGGAAATTCCTGCCGGAAGATGTTGAGACC 123
           |||||||||||||||| ||||| ||||| |||| ||| || ||||| |||||| |||||
Db   388 AAAAATTATGTGAATGACTGGTCCCTGAATTTCTGCCCAGAGATGTAGAGACA 329

Qy   124 AACTGTGAGTGGTCCGCCTTTCTCCTGTTTCCAGAAGAGCCAGCTGAAATCCGCAAACACC 183

RESULT 5
CD559457/c
LOCUS   CD559457   582 bp   mRNA   linear   EST 19-NOV-2003
DEFINITION   AGENCOURT 14496897 NIH_MGC_195 Homo sapiens cDNA clone
             IMAGE:6971865 5', mRNA sequence.
ACCESSION   CD559457
VERSION   CD559457.2 GI:38453482
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 582)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585525.
             Contact: Daniela S. Gerhard, Ph.D.
             http://image.llnl.gov
             Plate: IRBK2 row: g column: 08
             High quality sequence start: 5
             High quality sequence stop: 582.
FEATURES   Location/Qualifiers
     source   1..582
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971865"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene

Qy   328 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAGAGGCCCAACTAAAGTCAGCAAATACA 269
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTCAGAGAGGCCCAACTAAAGTCAGCAAATACA 269

Qy   184 GGTAACAACGAACGTATCATCAACAGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 GGTAACAACGAACGTATCATCAACAGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC 243

Qy   268 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC 209
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC 209

Qy   244 ACCAACGCAGGTCGTCGTCGACCTGACCTGCCCGGTCCTGTGATTCTTATGAG 303
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 ACAAATGCAGGGAGAAGACAGAAAACACGACTAACATGCCCTTCATGTGACTTATGAG 303

Qy   304 AAAAAACCGCCGAAAGAAATTCCTGGGAACGTTTCAAAATCCCTGCTGCCAGAAAAATGATTCAC 363
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   304 AAAAAACCGCCGAAAGAAATTCCTGGGAACGTTTCAAAATCCCTGCTGCCAGAAAAATGATTCAC 363

Qy   148 AAAAAAACCACCCAAAAGAAATTCCTAGAAAAGATTCAAAATCACTTCTCCAAAAAGATGATTCAT 89
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 AAAAAAACCACCCAAAAGAAATTCCTAGAAAAGATTCAAAATCACTTCTCCAAAAAGATGATTCAT 89

Qy   364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
                  ||||||||||||||||||||||||||||||||||||||||||
Db   88   CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 47

RESULT 6
CD559461/c
LOCUS   CD559461   582 bp   mRNA   linear   EST 19-NOV-2003
DEFINITION   AGENCOURT 14496648 NIH_MGC_195 Homo sapiens cDNA clone
             IMAGE:6971861 5', mRNA sequence.
ACCESSION   CD559461
VERSION   CD559461.2 GI:38453488
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 582)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585529.
             Contact: Daniela S. Gerhard, Ph.D.
             http://image.llnl.gov
             Plate: IRBK2 row: g column: 04
             High quality sequence start: 7

ORIGIN
Query Match   74.0%; Score 299.6; DB 5; Length 582;
Best Local Similarity   84.1%; Pred. No. 9.9e-83;
Matches 338; Conservative   0; Mismatches 64; Indels   0; Gaps   0;

Qy   4 CAAGGTCAAGAATCGGCCACACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
                  |||||||||||||| ||||| ||||||||||||||||||||||| ||||||||||||||||||
Db   449 CAAGGTCAAGAATCGGCCACATCATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 390

Qy   64 AAAAAATTATGTGAAATGACCTGGTTCCGGAAATTCCTGCCGGCGTTCCGGAAAGATTTGAGACC 123
                  |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   389 AAAAAATTATGTGAAATGACCTGGTTCCCTGAATTTCTCCCAGCTCCAGAAGAGATTAGAGACA 330

Qy   124 AACTGTGAGTGGTCCGCTTTCTCCGTGTTTCCAGAAAAGCCCAGCTGAAATCCGCCAAACC 183
                  ||||||||||||| ||||| |||| ||||||||||| |||||||||||||||| ||||||||
Db   329 AACTGTGAGTGGTCAGCTTTTTCCGTTTTCCGTTTTCAGAGAGGCCCAACTAAAGTCAGCAAATACA 270

Qy   184 GGTAACAACGAACGTATCATCAACAGTTTTCCATTAAAAAAACTGAAACGTAAACCGCCGTCC 243
                  |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   269 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC 210

Qy   244 ACCAACGCAGGTCGTCGTCGACAACAACCGTCTGACCTGCCCGGTCCTGTGATTCTTATGAG 303
                  |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   209 ACAAATGCAGGGAGAAGACAGAAAACACGACTAACATGCCCTTCATGTGACTTATGAG 150

Qy   304 AAAAAACCGCCGAAAGAAATTCCTGGGAACGTTTCAAAATCCCTGCTGCCAGAAAAATGATTCAC 363
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   149 AAAAAAACCACCCAAAAGAAATTCCTAGAAAAGATTCAAAATCACTTCTCCAAAAAGATGATTCAT 90

Qy   364 CAGCACCTGTCCTCTCGTACCCACGGTTCCGAAGATTCCTGA 405
                  ||||||||||||||||| |||||||| ||||||||||||||
Db   89   CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 48

Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

RESULT 7

LOCUS   CD559456   583 bp   mRNA   linear   EST   19-NOV-2003

DEFINITION AGENCOURT_14496960 NIH_MGC_195 Homo sapiens cDNA clone
           IMAGE:6971866 5', mRNA sequence.

ACCESSION   CD559456

VERSION   CD559456.2 GI:38453480

KEYWORDS   EST.

SOURCE   Homo sapiens (human)

ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.

REFERENCE   1 (bases 1 to 583)

AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL   Unpublished (1999)

COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585524.
           Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           National Cancer Institute / NIH
           Plate: IRBK2 row: g column: 09
           High quality sequence start: 8
           High quality sequence stop: 583.

FEATURES   Location/Qualifiers

source   1..583
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="IMAGE:6971866"
           /tissue_type="mixed"
           /lab_host="DH5A (T1 phage-resistant)"
           /clone_lib="NIH_MGC_195"
           /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
           loxP-HindIII; Clones from this library have been
           PCR-amplified using gene-specific primers to contain the
           complete open reading frame (based on known gene sequences
           available from NCBI's RefSeq). Template for PCR is cDNA
           derived from either pooled cytoplasmic polyA RNA from 30
           cells lines or pooled total RNA from 10 different tissues
           (from BD Biosciences/Clontech and Washington University).
           PCR products are directionally cloned into the loxP sites
           of the pDNR-Dual vector. Library constructed by Dr.
           Narayan Bhat, Earl Bere III and Hongling Liao (Gene
           Expression Laboratory, Research Technology Program, SAIC
           Frederick, NCI-Frederick, Frederick, MD 21702). For
           information on which gene each clone represents, please
           visit our anonymous ftp site at
           ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presV.dat
           a Note: this is a NIH_MGC Library."

ORIGIN

Query Match   74.0%; Score 299.6; DB 5; Length 583;
Best Local Similarity   84.1%;   Pred. No. 9.9e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
Qy      4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    450 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 391

Qy     64 AAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGCGGCTCCGGAAGATGTTGAGACC 123
          |||||||||||||||||||||||  ||||||||||||  ||  ||||||||||||||||||
Db    390 AAAAAATTATGTGAATGACTTGGTCCCCTGGAATTTCTGCCCAGCTCCCGGAAGATGTTGAGACA 331

Qy    124 AACTGTGAGTGGTCCGGCTTTTCTCCCGTTTCCCAGAAAGCCCAGCTGAAATCCGCAAACACC 183
          |||||||||||||  ||||||| ||| |||||  ||||| ||||  | |||||    ||| || 
Db    330 AACTGTGAGTGGTCAGCTTTTTCCTGTTTTTCAGAAGGCCCCAACTAAAAGTCACCAAAATACA 271

Qy    184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAACCGGCGTCC 243
          || |||||  |||  ||||| |||||| |||||||||||| ||||  | |||||  ||| ||
Db    270 GGAAACAATGAAAGGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAAACCACCTTCC 211

Qy    244 ACCAAGGCAGGTCGTTCGTTGGTCAGAAAACACGGTTCTGACCTGCCCGTCCCTGGTATTCTTATGAG 303
          || |||| ||| ||  | ||  |||||||||| |  | | |   | ||||||| || |||||||||||
Db    210 ACAAATGCAGGGAGGAAGACAGGAAACACAGACTAACATCGCCCTTCATGTGATTCTTATGAG 151

Qy    304 AAAAAACCGCCGAAAGAATTCCTGGAACGTTTCAAATCCCTGCTCGAGAAATGATTCAC 363
          ||||||| | | |||||||||| |||  | ||||||| | ||  || ||| ||||||| 
Db    150 AAAAAACACCCAAAGAATTCCTAGAAAGAATTCAAATCACTTCTCAAAAGATGATTCAT 91

Qy    364 CAGCACCTGTCCTCTCTGTACCCACGGTTCCGGAGGATTCCTGA 405
          ||||| |||||||||  |  ||| |||  | || |  |||||||
Db     90 CAGCATCTGTCCTCTAGAACACACGGCGAAGTGAAGAATTCCTGA 48
```

RESULT 7

LOCUS   CD559456   583 bp   mRNA   linear   EST   19-NOV-2003

DEFINITION AGENCOURT_14496960 NIH_MGC_195 Homo sapiens cDNA clone
           IMAGE:6971866 5', mRNA sequence.

ACCESSION   CD559456

VERSION   CD559456.2 GI:38453480

KEYWORDS   EST.

SOURCE   Homo sapiens (human)

ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
Qy    304  AAAAAACCCGCGGGAAAGAATTCCTCGGAAACGTTTCAAATCCTCTGCTTGCAGAAAATGATTCAC 363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150  AAAAAACACCCAAAGAGAATTCCTAGAAAGAGATTCAAATCACTTCTCCAAAAGATGATTCAT 91

Qy    364  CAGCACCTGTCCTCTCGTACCACGGTTCCGAAGAATTCCTGA 405
           ||||||||||||||||||||||||||||||||||||||||
Db    90   CAGCATCTGTTCCTCTAGAACACACCGGAAGTGAAGAGATTCCTGA 49
```

RESULT 8
CD559612

LOCUS   CD559612   583 bp   mRNA   linear   EST 26-NOV-2003
DEFINITION AGENCOURT_14496744 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971863 5', mRNA sequence.
ACCESSION   CD559612
VERSION   CD559612.2 GI:38558948
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo
REFERENCE   1 (bases 1 to 583)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585680.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2 row: g column: 06
            High quality sequence stop: 583.
FEATURES   Location/Qualifiers
     source   1..583
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971863"
                     /tissue_type="mixed"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

Query Match   74.0%; Score 299.6; DB 5; Length 583;
Best Local Similarity   84.1%; Pred. No. 9.9e-83;
Matches 338; Conservative   0; Mismatches 64; Indels   0; Gaps   0;
```

```
Qy      4  CAAGGTCAAGATCGCCACCATGATTAGAAATGGCTCAACTTATTATTGTTGATCAGCTG 63
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151  CAAGGTCAAGATCGCCACACATGATTAGAAATGGGTCAACTTATAGATATTGTTGATCAGCTG 210

Qy     64  AAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCGCGGTCCGGAAGATGTTGAGACC 123
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211  AAAAAATTATGTGAATGACTTGGTCCCTGAATTTCTGCGCAGGTCCAGAGAGATGTAGAGGACA 270

Qy    124  AACTGTGAGTGGTCCGCTTTCTCCGTTTCCAGAAAAGACCACCAGCTGAAAATCCGCAAACACC 183
           ||||||||||||||||| ||| |||||||||||||||| ||||||||||| || ||||
Db    271  AACTGTGAAGTGGTCAGCTTTTCCCGTTTTCAGAAGGCCCCAACTAAAAGTCAGGAAATACA 330

Qy    184  GGTAACAACGAACGAACGTTATCATCAACGTTTCCATTAAAAAACTGAAAACGTAAACCGCCGTCC 243
           ||||||||||||| ||| ||||||||||||||||| ||||||||||||||||||||||
Db    331  GGAAACAAATGAAAAGATTAATCATAACTTGGTCCCTGAAATTAAAAAAGCTGAAAACCACACTTCC 390

Qy    244  ACCAACGCAGGTCGTCGTCAGAAACACCGGTCCGCCGTCCCTGTGATTCTTATGAG 303
           |||||||||| ||||||||||||||||||| |||||||||| ||| | ||||||||
Db    391  ACAAATGCAGGGAGAGGAGAAACACAGAAGACTAACACGTCCCTTCATCTGATTCTTTATGAG 450

Qy    304  AAAAAACCGCGGAAAGAATTCCTGGAACGTTTCAAATCCCTCCGCTGCAGAAAATGATTCAC 363
           ||||||||||||||||||||| ||||||||||||||||||| ||| ||||||||||||
Db    451  AAAAAACCACCCAAAGAGAATTCCTAGAAAGAGATTCAAATCACTTCTCCAAAAGATGATTCAT 510

Qy    364  CAGCACCTGTCCTCTCGTACCACGGTTCCGAAGAATTCCTGA 405
           |||||||||||||||||||||||||||||||||||||||||
Db    511  CAGCATCTGTTCCTCTAGAACACACCGGAAGTGAAGAGATTCCTGA 552
```

RESULT 9
CD559614

LOCUS   CD559614   592 bp   mRNA   linear   EST 26-NOV-2003
DEFINITION AGENCOURT_14496629 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971861 5', mRNA sequence.
ACCESSION   CD559614
VERSION   CD559614.2 GI:38558951
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 592)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585682.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2 row: g column: 04
            High quality sequence stop: 592.
FEATURES   Location/Qualifiers
     source   1..592
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971861"
                     /tissue_type="mixed"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxp-HindIII; Clones from this library have been
```

RESULT 10

```
LOCUS       CD559610                 599 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496869 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971865 5', mRNA sequence.
ACCESSION   CD559610
VERSION     CD559610.2  GI:38558945
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585678.
            Contact: Daniela S. Gerhard, Ph.D.
            National Cancer Institute / NIH
            Office of Cancer Genomics
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
```

Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

```
FEATURES             Location/Qualifiers
     source          1..599
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971865"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."
                     /tissue_type="mixed"
                     High quality sequence start: 13
                     High quality sequence stop: 599.
                     Plate: IRBK2 row: g column: 08
```

ORIGIN

```
Query Match  74.0%;  Score 299.6;  DB 5;  Length 592;
Best Local Similarity  84.1%;  Pred. No. 1e-82;
Matches 338;  Conservative  0;  Mismatches  64;  Indels  0;  Gaps  0;

Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATATGTTGATCAGCTG   63
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  158 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATATGTTGATCAGCTG  217

Qy   64 AAAAAATTATGTGAAATGACCTGGTTCCGGAAATTCCTGCCGGTCCGGAAGAAGTTGAGACC  123
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  218 AAAAAATTATGTGAAATGACCTGGTTCCGGAAATTCCTGCCGGTCCGGAAGAAGTTGAGACA  277

Qy  124 AACTGTGAGTGGTGCTCAGCTTTTTCCCTGTTTCAGAGAAGCCCAGCTGAAATCCCAAACC  183
        ||||||||||||||||||||||||||||||||||||||||||
Db  278 AACTGTGAGTGGTCAGCTTTTTCCCTGTTTCAGAGAAGCCCAACTAAAAGTCACCAAAATACA  337

Qy  184 GGTAACAACGAACGTATCATCCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC  243
        |||||||||  ||||||  ||||||||||
Db  338 GGAAACAAATGAAAGGATTAATCAATGTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC  397

Qy  244 ACCAACGCAGGTCGTCGTCAGAAACACCGTTCGACCTGCCCGTCCGTTGATTCTTATGAG  303
        ||   ||||||  || |||||||| ||||| |||| ||||||||||||||||
Db  398 ACAAATGCAGGGAGGAAGACAGAAAACAGATAAACATGCCCTTCATGTGATTTCTTATGAG  457

Qy  304 AAAAAAACCGCCGGAAAAGAAATTCCCTGGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC  363
        ||||||  |||  ||||||||||||  || ||||||||||| || |||  |||||||||||||
Db  458 AAAAAACCCCAAAAGAAATTCCTAGAAAAGAATTCAAATCACTTCTCCAAAAGAGTAGATTCAT  517

Qy  364 CAGCACCTGCTCCTCTCGTTACCCACGGTTCCGGAAGAAGATTCCTGA  405
        |||||  ||| ||| |||||||||||  |||| ||||||||||||||||
Db  518 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA  559
```

RESULT 11

```
LOCUS       CD559613
ACCESSION   CD559610
```

ORIGIN

```
Query Match  74.0%;  Score 299.6;  DB 5;  Length 599;
Best Local Similarity  84.1%;  Pred. No. 1e-82;
Matches 338;  Conservative  0;  Mismatches  64;  Indels  0;  Gaps  0;

Qy    4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATATGTTGATCAGCTG   63
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  165 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATATGTTGATCAGCTG  224

Qy   64 AAAAAATTATGTGAAATGACCTGGTTCCGGAAATTCCTGCCGGTCCGGAAGAAGTTGAGACC  123
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  225 AAAAAATTATGTGAAATGACCTGGTTCCGGAAATTCCTGCCGGTCCGGAAGAAGTTGAGACA  284

Qy  124 AACTGTGAGTGGTGCTCAGCTTTTTCCCTGTTTCAGAGAAGCCCAGCTGAAATCCCAAACC  183
        |||||||||||||||||||||||||||||||||||||||||
Db  285 AACTGTGAGTGGTGCTCAGCTTTTTCCCTGTTTCAGAGAAGCCCAACTAAAAGTCACCAAAATACA  344

Qy  184 GGTAACAACGAACGTATCATCCAACGTTTCCATTAAAAAACTGAAACGTAAACCGCCGTCC  243
        ||||||||  ||||||  |||||||||
Db  345 GGAAACAAATGAAAGGATTAATCAATGTATCAATTAAAAAGCTGAAGAGGAAAACCACCTTCC  404

Qy  244 ACCAACGCAGGTCGTCGTCAGAAACACCGTTCGACCTGCCCGTCCGTTGATTCTTATGAG  303
        ||  ||||||  || ||||||||||| |||| ||||||||||||||||
Db  405 ACAAATGCAGGGAGGAAGACAGAAAACAGATAAACATGCCCTTCATGTGATTTCTTATGAG  464

Qy  304 AAAAAAACCGCCGGAAAAGAAATTCCCTGGGAACGTTTCAAAATCCCTGCTGCAGAAAATGATTCAC  363
        ||||||  |||  ||||||||||| || ||||||||||| || |||  ||||||||||||
Db  465 AAAAAACCCCAAAAGAAATTCCTAGAAAAGAATTCAAATCACTTCTCCAAAAGAGTAGATTCAT  524

Qy  364 CAGCACCTGCTCCTCTCGTTACCCACGGTTCCGGAAGAAGATTCCTGA  405
        |||||  ||| ||| ||||||||||||  |||| ||||||||||||||||
Db  525 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA  566
```

```
LOCUS       CD559613                 600 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496682 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971862 5', mRNA sequence.
ACCESSION   CD559613
VERSION     CD559613.2  GI:38558920
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585681.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2 row: g column: 05
            High quality sequence start: 14
            High quality sequence stop: 600.
FEATURES             Location/Qualifiers
     source          1..600
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971862"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC library."

ORIGIN

Query Match           73.6%;  Score 298;  DB 5;  Length 600;
Best Local Similarity 83.8%;  Pred. No. 3.2e-82;
Matches 337;  Conservative 0;  Mismatches 65;  Indels 0;  Gaps 0;

Qy    4 CAAGTCAAGATCCGCCACATGATTAGAAATCCGTCAACTTATAGATATTGTTGATCAGCTG 63
         |||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  166 CAAGGTCAAGATCCGCCACATGATTAGAATCGGTCAACTTATAGATATTGTTGATCAGCTG 225

Qy   64 AAAAATTATGTGAATGAACTGGTTCCGGAATTCCTGCGGTTCCGGAAGAGTTGAGACC 123
         ||||||||||||||||||  ||||||||| ||||| |||   | || ||||| || ||
Db  226 AAAAATTATGTGAATGACTTGGTTCCCTGAATTTCTGCCGCAGCTCCAGAAGAGTTAGAGACA 285

Qy  124 AACTGTGAGTGTCGGTCCGCCTTTCTCCGTGTTTCCAGAAAGCCCAGCTGAAATCCGCAAAACACC 183
         |||||||||||| ||||  |||||| || |||||||| || ||| ||||  |  ||  |||  ||
```

```
Db  286 AACTGTGAGTGTGGTCAGCTTTTTCCTGCGTTTCAGAAGCGCCCAACTAAAGTCAGCAAATACA 345

Qy  184 GGTAACAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAACGTAAACGGCGTCC 243
         || |||||| ||| ||||||||||||| |||| |||||| |||||  | | | ||| |||
Db  346 GGAAACAAATGAAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGAAACCACCTTCC 405

Qy  244 ACCAAGCGCAGGTCGTCGTGCTCAGAAAACACCGTCTGACCTGCCGGTCCGTCTGTGATTCTTATGAG 303
         ||| | ||| |||  |  | |||||||||| |||| || ||||   | || | ||||| |||||| ||
Db  406 ACAAATGCAGGGAGGAAGAAGAACAGAAACACAGACTAACATGCCCTTCACGTGATCTTATCAT 465

Qy  304 AAAAAACCGGCCGAAAGAGAATTCCTTGGAACGTTTCAAAATCCCTGCGTGCAGAAAATGATTCAC 363
         ||||||||  | |||||||||||||| |||| | | |||||||  | ||||| |||||||||||| |
Db  466 AAAAAAACCACCCCAAAGAATTCCTTAGGAAAGATTCAAACACATCTTCCAAAAAGATGATTCAT 525

Qy  364 CAGCACCTGTCCTCTCCGTACCCCACGGTTCCGAAGAGTCCTGA 405
         |||| | ||||||||| | ||| | ||| | ||||||||||||
Db  526 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGAGATTCCTGA 567
```

RESULT 12
CD559460/c

```
LOCUS       CD559460                 581 bp    mRNA    linear   EST 19-NOV-2003
DEFINITION  AGENCOURT_14496710 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971862 5', mRNA sequence.
ACCESSION   CD559460
VERSION     CD559460.2  GI:38453455
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 581)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585528.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK2 row: g column: 05
            High quality sequence start: 4
            High quality sequence stop: 581.
FEATURES             Location/Qualifiers
     source          1..581
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971862"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program,
```

FEATURES   Location/Qualifiers
COMMENT   This sequence was made by sequencing genomic exons and ordering
                        them based on alignment
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                        Rockville, MD 20850, USA
REFERENCE   2 (bases 1 to 489)
PUBMED   1471302
JOURNAL   Science 302 (5652), 1960-1963 (2003)
                        Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
                        gene trios
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                        Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                        Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
REFERENCE   1 (bases 1 to 489)
ORGANISM   Pan troglodytes
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                        Hominidae; Pan.
SOURCE   Pan troglodytes (chimpanzee)
KEYWORDS   GSS.
VERSION   AY417616.1 GI:39773576
ACCESSION   AY417616
DEFINITION   Pan troglodytes IL21 gene, VIRTUAL TRANSCRIPT, partial sequence,
                        genomic survey sequence.
LOCUS   AY417616   489 bp   DNA   linear   GSS 17-DEC-2003
RESULT 13

Matches 336; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
Best Local Similarity 83.6%; Pred. No. 1e-81; DB 5;
Query Match 73.2%; Score 296.4; Length 581;

ORIGIN

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 389

Qy   64 AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGGCTCCGGAAGAGTTGAGACC 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 AAAAATTATGTGAATGACTTGGTCCCTGAATTTCTCCAGAAGAGTTAGAGACA 329

Qy   124 AACTGTGAGTGGTTCCGGCTTTTCTCCCTGTTTCCAGAGTGAAATCCGCAAACACC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 AACTGTGAGTGGTTCAGCTTTTTTCCTGCTTTCAGAAGGCCCCAACTAAAGTCAGCAAATACA 269

Qy   184 GGTAACAAACGAACGTATCATCAACGTTTCCATTAAAAAAACTGAAAACGTAAAAACCCCCGTCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 GGAAACAAATGAAAAGGAATAAATCAATGTTATCAATTAAAAAGCTGAAGAGGGAAAAACCACCTTCC 209

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAACACACCGGTCTCGGACCTGCCCGTCCCGTGGTCGTGGTTCTTATGAG 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 ACAAATGCAGGGAGGAGAGAGAGAGAAATTCCTGGAAACGTTTCAAAATCCTGCTGCACGAAAAAATGATTCAC 149

Qy   304 AAAAAACCGCCGAAAGAAATTCCTAGAAAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 AAAAAACCACCCAAAGAAATTCCTAGAAAAGAATTCAAAATCACTTCTCCAAAAGATGATTCAT 89

Qy   364 CAGCACCCTGTCCTCCGTACCCACGGTTCCGGAAGATTCCTGA 405
          |||||||||||||||||||||||||||||||||||||||
Db   88 CAGAATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 47

RESULT 14

Matches 332; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Best Local Similarity 82.6%; Pred. No. 4.8e-81; DB 14;
Query Match 72.6%; Score 294.2; Length 489;

ORIGIN

Qy   4 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 CAAGGTCAAGATCGCCACATGATTAGAATGCGTCAACTTATAGATATTGTTGATCAGCTG 147

Qy   64 AAAAATTATGTGAATGACCTGGTT CCGGAATTCCTGCCGGCTCCGGAAGAGTTGAGACC 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 AAAAATTATGTGAATGACTTGGGTCCCTGAATTTTCTGCCAGCTCCAGAAGAGTTAGAGACA 207

Qy   124 AACTGTGAGTGGTTCCGGCTTTTCTCCCTGTTTCCAGAGTGAAATCCGCAAACACC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 AACTGTGAGTGGTTCAGCTTTTTTCCTGCTTTCAGAAGGCCCCAACTAAAGTCAGCAAATACA 267

Qy   184 GGTAACAAACGAACGTATCATCAACGTTTCCATTAAAAAACTGAAAACGTAAAAACCCCCGTCC 243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 GGTAACAAATGAAAAGGAATAAATCAATGTTATCAATTAAAAAGAGCCCAACTAAAAGTCAGCAAATACA 327

Qy   244 ACCAACGCAGGTCGTCGTTCAGAAACACACCGTCTCGACCTGCCCGTCCCGTGGTTCTTATGAG 303
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 ACAAATGCAGGGAGGAGAGAGAGAGAAATTCCTGGAAACGTTTCAAAATCCTGCTGCACGAAAAAATGATTCAC 387

Qy   304 AAAAAACCGCCGAAAGAAATTCCTGGAAACGTTTCAAAATCCCTGCTGCACGAAAAAATGATTCAC 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 AAAAACNNNNCAAAAGAAATTCCTAGAAAAGATTCAAAATCACTTCTCCAAAAGATGATTCAT 447

Qy   364 CAGCACCCTGTCCTCCGTACCCACGGTTCCGGAAGATTCCTGA 405
          ||||||||||||||||||||||||||||||||||||||||
Db   448 CAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA 489

LOCUS   CR988723   551 bp   mRNA   linear   EST 28-JUN-2005
DEFINITION   CR988723 RZPD no.9016 Homo sapiens cDNA clone RZPDp9016J0144 5',
                        mRNA sequence.
ACCESSION   CR988723
VERSION   CR988723.1 GI:68282608
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                        Hominidae; Homo.
REFERENCE   1 (bases 1 to 551)
AUTHORS   Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
                        and Korn,B.
TITLE   Human T-Lymphocytes library
JOURNAL   Unpublished (2005)
COMMENT   Contact: Inge Arlart
                        RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
                        Heubnerweg 6, D-14059 Berlin, Germany
                        Email: www.rzpd.de
                        RZPD; RZPDp9016J0144.
                        RZPDlib: (Human T-Lymphocytes) RZPD LIB No.9016 Contact:
                        http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016
                        Inge Arlart
                        RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
                        Heubnerweg 6, D-14059 Berlin, Germany
                        Tel: +49 30 32639 100
                        Fax: +49 30 32639 111
                        www.rzpd.de

ORIGIN

          1. .489
          /organism="Pan troglodytes"
          /mol_type="genomic DNA"
          /db_xref="taxon:9598"

gene   <1. .>489
          /gene="IL21"
          /locus_tag="HCM6283"

source   Frederick, NCI-Frederick, Frederick, MD 21702). For
          information on which gene each clone represents, please
          visit our anonymous ftp site at
          ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presV.dat
          a Note: this is a NIH_MGC library."

Left column

```
           This clone is available from RZPD;
           http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD90160144
           contact RZPD (product-support@rzpd.de) for further information.
           Primer name: qe3.4 , Primer sequence: CGGATAACAATTCACACAG.
FEATURES             Location/Qualifiers
     source          1..551
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="RZPD90160144"
                     /tissue_type="T-Lymphocytes"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RZPD no.9016"
                     /note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
                     NotI; Vector:
                     http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
                     ; 1st strand cDNA was prepared from mRNA obtained from
                     human T-Lymphocytes with a NotI - oligo(dT) primer [5'
                     GACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to SalI adaptors,
                     digested with NotI and cloned into the NotI and SalI sites
                     of the pQE80LSN_cloned vector"
ORIGIN

Query Match        72.2%;  Score 292.6;  DB 8;  Length 551;
Best Local Similarity  82.3%;  Pred. No. 1.6e-80;
Matches 331;  Conservative  0;  Mismatches 71;  Indels  0;  Gaps  0;

Qy      4  CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATTGTTGATCAGCTG   63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139  CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATTGTTGATCAGCTG  198

Qy     64  AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGCCGCTCCGGAAGAGTTGAGACC  123
           ||||| || |||| ||| ||||||||||||||||||||||||||| ||||||| |||||||
Db    199  AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGCCGCTCCAGAAGAGTTAGAGACA  258

Qy    124  AACTGTGAGTGGTCCGGCTTTCTCCTGTTTCCCAGGAAAGCCCAGCTGAAATCCGACAAACACC  183
           |||||| || |||||  |||| ||||||||| ||| |||||||| || ||| |   |||| | |
Db    259  AACTGNGAGTGGTCAGCTTTTTCCTGTTTTCAGAAGGGCCCAACTAAAGTCANCAAAATACA  318

Qy    184  GGTAACAACGAAACGTATCATCAACGTTTCCATTAAAAACTGAAACGTAAACGCCGGTCC  243
           || |||||| |||| ||| ||||| ||| | ||||||| ||||| | ||||  |||| ||
Db    319  GGAAACAATGAAAAGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACCTTCC  378

Qy    244  ACCAAACGCAGGTCGTCGTCAGAAACACACCGTCTGACCTGCCCGTCCTGTGATTCTTATGAG  303
           || ||  |||| |   | ||||| |||| | ||| |||| |||| |  | |||||||||||||
Db    379  ACNAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATTCTTATGAA  438

Qy    304  AAAAAACCCGCGAAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTCAGAAAATGATTCAC  363
           |||||| | || |||||||||||  |||||| |||||||||||  |||| |  |||||||
Db    439  AAAAAAACCACCCGAAAAGAAATTCCACTTCTCCAAAAGATGATTCAT  498

Qy    364  CAGCACCTGTTCCTTCTCTGCGTTCCGAAGGATTCCTGA  405
           ||| || ||| ||| ||       |||| |  | ||| ||
Db    499  CANNATCTGTCCTCTANAACACACGGAAGTGAAAANAATTCCTGA  540
```

Right column

```
                     National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE
  JOURNAL    Unpublished (1999)
  COMMENT    On Jun 10, 2003 this sequence version replaced gi:31585679.
             Contact: Daniela S. Gerhard, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Narayan Bhat
             National Cancer Institute / NIH
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: IRBK2    row: g    column: 07
             High quality sequence start: 14
             High quality sequence stop: 608.
FEATURES             Location/Qualifiers
     source          1..608
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971864"
                     /tissue_type="mixed"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC library."
ORIGIN

Query Match        69.9%;  Score 283.2;  DB 5;  Length 608;
Best Local Similarity  82.7%;  Pred. No. 1.5e-77;
Matches 339;  Conservative  0;  Mismatches 63;  Indels  8;  Gaps  1;

Qy      4  CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATTGTTGATCAGCTG   63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166  CAAGGTCAAGATCGCCACATGATTAGAATGGCTCAACTTATAGATATTGTTGATCAGCTG  225

Qy     64  AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGCCGCTCCGGAAGAGTTGAGACC  123
           ||||| || |||| |||||||||||||||||||||||||||||||| ||||||| |||||
Db    226  AAAAATTATGTGAATGACCTGGTTCCGGAATTCCTGCCGCCGCTCCGGAAGAGTTTGAGACC  285

Qy    124  AACTGTGAGTGGTCCGGCTTTCTCCTGTTTCCCAGGAAAGCCCAGCTGAAATCCGACAAACACC  183
           ||| || ||||||| || ||||||||||||| ||||||||||||||||||||||||||||||
Db    286  AACTGTGAGTGGTCAGCTTTTTTCCTGTTTTCATTAAAAAACTGAAAACTGAAAACGCCCAAAATACA  345

Qy    184  GGTAACAACGAAACGTATCATCAACGTTTCCATTAAAAAACTGAAAAACTGAAAACGCCCAAAATACA  243
           || ||||| |||  |||  ||||| ||||||||  || |||||
Db    346  GGAAACAATGAAAAGATAATCAATGTATCAATTAAAAAAGCTGAAGAGGAAACCACCTTCC  405

Qy    244  ACCAAACGCAGGTCGTCGTCAGAAACACCGTCT--------GACCTGCCCGTCCTGTGATT  295
           || ||  |||| |   | ||||| |||| |            ||||| ||| ||  |||||
Db    406  ACAAATGCAGGGAGAAGACAGAAACACAGACTAACATGCCCTTCATGTGATT  465

Qy    296  CTTATGAGAAAAAACCCGCGAAAAGAAATTCCTGGAACGTTTCAAATCCCTGCTCAGAAAA  355
           |||||||||||||| | || |||||||||||  || |  ||  ||||| | || | |||||
Db    466  CTTATGAGAAAAAACCACCCGAAAAGAAATTCCCTCCCTTGCTTCAAATCACTTCTCCAAAAGA  525
```

```
Qy    356 TGATTCACCAGCACCTGTCCTCGTACCCACGGGTTCCGAAGATTCCTGA  405
          ||||||||| ||||||||||||| | || ||||||         |||||||||||||
Db    526 TGATTCATCAGCATCTGTCCTCTAGAACACACGGAAGTGAAGATTCCTGA  575
```

Search completed: August 7, 2006, 13:37:22
Job time : 4434 secs

THIS PAGE LEFT BLANK